

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
LEONARD, AMANDA

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS

(iii) NUMBER OF SEQUENCES: 40

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) (B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGACACTCCT TCCTTCTTCT CACCCGTCCT AGTCCCCTTC AACCCCCCTC TTTGACAAAG

60

5 ACAACAAACC ATGGCTGCTG CTCCCAGTGT GAGGACGTTT ACTCGGGCCG AGGTTTTGAA 120
 TGCCGAGGCT CTGAATGAGG GCAAGAAGGA TGCCGAGGCA CCCTTCTTGA TGATCATCGA 180
 CAACAAGGTG TACGATGTCC GCGAGTTCGT CCCTGATCAT CCCGGTGGAA GTGTGATTCT 240
 CACGCACGTT GGCAAGGACG GCACTGACGT CTTTGACACT TTTCACCCCG AGGCTGCTTG 300
 10 GGAGACTCTT GCCAACTTTT ACGTTGGTGA TATTGACGAG AGCGACCGCG ATATCAAGAA 360
 TGATGACTTT GCGGCCGAGG TCCGCAAGCT GCGTACCTTG TTCCAGTCTC TTGGTTACTA 420
 CGATTCTTCC AAGGCATACT ACGCCTTCAA GGTCTCGTTC AACCTCTGCA TCTGGGGTTT 480
 15 GTCGACGGTC ATTGTGGCCA AGTGGGGCCA GACCTCGACC CTCGCCAACG TGCTCTCGGC 540
 TGCGCTTTTG GGTCTGTTCT GGCAGCAGTG CGGATGGTTG GCTCACGACT TTTTGCATCA 600
 20 CCAGGTCTTC CAGGACCGTT TCTGGGGTGA TCTTTTCGGC GCCTTCTTGG GAGGTGTCTG 660
 CCAGGGCTTC TCGTCCTCGT GGTGGAAGGA CAAGCACAACT ACTCACCACG CCGCCCCCAA 720
 CGTCCACGGC GAGGATCCCG ACATTGACAC CCACCCTCTG TTGACCTGGA GTGAGCATGC 780
 25 GTTGGAGATG TTCTCGGATG TCCCAGATGA GGAGCTGACC CGCATGTGGT CGCGTTTCAT 840
 GGTCTGAAC CAGACCTGGT TTTACTTCCC CATTCTCTCG TTTGCCCGTC TCTCTGGTG 900
 30 CCTCCAGTCC ATTCTCTTTG TGCTGCCTAA CGGTCAGGCC CACAAGCCCT CGGGCGCGCG 960
 TGTGCCCATC TCGTTGGTCG AGCAGCTGTC GCTTGCATG CACTGGACCT GGTACCTCGC 1020
 CACCATGTTC CTGTTTCATCA AGGATCCCGT CAACATGCTG GTGTACTTTT TGGTGTGCGA 1080
 35 GGCGGTGTGC GGAAACTTGT TGGCGATCGT GTTCTCGCTC AACCACAACG GTATGCCTGT 1140
 GATCTCGAAG GAGGAGGCGG TCGATATGGA TTTCTTCACG AAGCAGATCA TCACGGGTCG 1200
 40 TGATGTCCAC CCGGGTCTAT TTGCCAACTG GTTCACGGGT GGATTGAACT ATCAGATCGA 1260
 GCACCACTTG TTCCCTTCGA TGCCTCGCCA CAACTTTTCA AAGATCCAGC CTGCTGTGCA 1320
 GACCCTGTGC AAAAAGTACA ATGTCCGATA CCACACCACC GGTATGATCG AGGGAACCTGC 1380
 45 AGAGGTCTTT AGCCGTCTGA ACGAGGTCTC CAAGGCTGCC TCCAAGATGG GTAAGGCGCA 1440
 GTAAAAAAA AAACAAGGAC GTTTTTTTTC GCCAGTGCCT GTGCCTGTGC CTGCTTCCCT 1500
 50 TGTCAAGTCG AGCGTTTCTG GAAAGGATCG TTCAGTGCAG TATCATCATT CTCCTTTTAC 1560
 CCCCCGCTCA TATCTCATTC ATTTCTCTTA TTAACAACCT TGTTCCCCC TTCACCG 1617

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu
 1 5 10 15
 Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
 20 25 30
 10 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
 35 40 45
 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
 50 55 60
 15 Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
 65 70 75 80
 Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
 85 90 95
 20 Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
 100 105 110
 25 Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
 115 120 125
 Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
 130 135 140
 30 Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
 145 150 155 160
 Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
 165 170 175
 35 His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
 180 185 190
 40 Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
 195 200 205
 His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
 210 215 220
 45 Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
 225 230 235 240
 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
 245 250 255
 50 Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
 260 265 270
 55 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
 275 280 285
 Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
 290 295 300
 60 Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
 305 310 315 320
 Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser
 325 330 335
 65 Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His

340 345 350
 Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe
 355 360 365
 5 Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe
 370 375 380
 10 Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
 385 390 395 400
 Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val
 405 410 415
 15 Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met
 420 425 430
 Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys
 435 440 445
 20 Ala Ala Ser Lys Met Gly Lys Ala Gln
 450 455

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1488 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40 GTCCCCTGTC GCTGTGCGCA CACCCCATCC TCCCTCGCTC CCTCTGCGTT TGTCCCTTGGC 60
 CCACCGTCTC TCCTCCACCC TCCGAGACGA CTGCAACTGT AATCAGGAAC CGACAAATAC 120
 ACGATTTCTT TTTACTCAGC ACCAACTCAA AATCCTCAAC CGCAACCCTT TTTCAGGATG 180
 45 GCACCTCCCA AACTATCGA TGCCGGTTTG ACCCAGCGTC ATATCAGCAC CTCGGCCCCA 240
 AACTCGGCCA AGCCTGCCTT CGAGCGCAAC TACCAGCTCC CCGAGTTCAC CATCAAGGAG 300
 50 ATCCGAGAGT GCATCCCTGC CCACTGCTTT GAGCGCTCCG GTCTCCGTGG TCTCTGCCAC 360
 GTTGCCATCG ATCTGACTTG GGCCTCGCTC TTGTTCCTGG CTGCGACCCA GATCGACAAG 420
 TTTGAGAATC CCTTGATCCG CTATTTGGCC TGGCCTGTTT ACTGGATCAT GCAGGGTATT 480
 55 GTCTGCACCG GTGTCTGGGT GCTGGCTCAC GAGTGTGGTC ATCAGTCCTT CTCGACCTCC 540
 AAGACCCTCA ACAACACAGT TGTTGGATC TTGCACTCGA TGCTCTTGGT CCCCTACCAC 600
 TCCTGGAGAA TCTCGCACTC GAAGCACCAC AAGGCCACTG GCCATATGAC CAAGGACCAG 660
 60 GTCTTTGTGC CCAAGACCCG CTCCCAGGTT GGCTTGCTC CCAAGGAGAA CGTGCTGTCT 720
 GCCGTTTCTG AGGAGGACAT GTCCGTGCAC CTGGATGAGG AGGCTCCCAT TGTGACTTTG 780
 65 TTCTGGATGG TGATCCAGTT CTTGTTCGGA TGGCCCGCGT ACCTGATTAT GAACGCCTCT 840

5 GGCCAAGACT ACGGCCGCTG GACCTCGCAC TTCCACACGT ACTCGCCCAT CTTTGAGCCC 900
 CGCAACTTTT TCGACATTAT TATCTCGGAC CTCGGTGTGT TGGCTGCCCT CGGTGCCCTG 960
 10 ATCTATGCCT CCATGCAGTT GTCGCTCTTG ACCGTCACCA AGTACTATAT TGTCCCCTAC 1020
 CTCTTTGTCA ACTTTTGGTT GGTCTGATC ACCTTCTTGC AGCACACCGA TCCCAAGCTG 1080
 CCCCATTACC GCGAGGGTGC CTGGAATTTT CAGCGTGGAG CTCTTTGCAC CGTTGACCGC 1140
 TCGTTTGGCA AGTTCTTGA CCATATGTTT CACGGCATTG TCCACACCCA TGTGGCCCAT 1200
 CACTTGTCTT CGCAAATGCC GTTCTACCAT GCTGAGGAAG CTACCTATCA TCTCAAGAAA 1260
 15 CTGCTGGGAG AGTACTATGT GTACGACCCA TCCCGATCG TCGTTGCGGT CTGGAGGTCG 1320
 TTCCGTGAGT GCCGATTCTG GGAGGATCAG GGAGACGTGG TCTTTTCAA GAAGTAAAAA 1380
 AAAAGACAAT GGACCACACA CAACCTTGTC TCTACAGACC TACGTATCAT GTAGCCATAC 1440
 20 CACTTCATAA AAGAACATGA GCTCTAGAGG CGTGTCAATC GCGCCTCC 1488

(2) INFORMATION FOR SEQ ID NO:4:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: peptide
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
 40 Met Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile
 1 5 10 15
 Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr
 20 25 30
 45 Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
 35 40 45
 His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
 50 55 60
 Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp
 65 70 75 80
 55 Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
 85 90 95
 Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
 100 105 110
 60 Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val
 115 120 125
 Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg
 130 135 140
 65 Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp
 145 150 155 160

5 Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys
 165 170 175
 10 Glu Asn Ala Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu
 180 185 190
 15 Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe
 195 200 205
 20 Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp
 210 215 220
 25 Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu
 225 230 235 240
 30 Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala
 245 250 255
 35 Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr
 260 265 270
 40 Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu
 275 280 285
 45 Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr
 290 295 300
 50 Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp
 305 310 315 320
 55 Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
 325 330 335
 60 Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
 340 345 350
 65 Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
 355 360 365
 70 Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu
 370 375 380
 75 Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
 385 390 395

(2) INFORMATION FOR SEQ ID NO:5:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Glu Val Arg Lys Leu Arg Thr Leu Phe Gln Ser Leu Gly Tyr Tyr Asp
 1 5 10 15
 Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val Ser Phe Asn Leu Cys Ile
 20 25 30

5 Trp Gly Leu Ser Thr Val Ile Val Ala Lys Trp Gly Gln Thr Ser Thr
 35 40 45
 Leu Ala Asn Val Leu Ser Ala Ala Leu Leu Gly Leu Phe Trp Gln Gln
 50 55 60
 10 Cys Gly Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Gln Asp
 65 70 75 80
 Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe Leu Gly Gly Val Cys Gln
 85 90 95
 15 Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys His Asn Thr His His Ala
 100 105 110
 Ala Pro Asn Val His Gly Glu Asp Pro Asp Ile Asp Thr His Pro Leu
 115 120 125
 20 Leu Thr Trp Ser Glu His Ala Leu Glu Met Phe Ser Asp Val Pro Asp
 130 135 140
 25 Glu Glu Leu Thr Arg Met Trp Ser Arg Phe Met Val Leu Asn Gln Thr
 145 150 155 160
 Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala Arg Leu Ser Trp Cys Leu
 165 170 175
 30 Gln Ser Ile Leu Phe Val Leu Pro Asn Gly Gln Ala His Lys Pro Ser
 180 185 190
 Gly Ala Arg Val Pro Ile Ser Leu Val Glu Gln Leu Ser Leu Ala Met
 195 200 205
 35 His Trp Thr Trp Tyr Leu Ala Thr Met Phe Leu Phe Ile Lys Asp Pro
 210 215 220
 Val Asn Met Leu Val Tyr Phe Leu Val Ser Gln Ala Val Cys Gly Asn
 225 230 235 240
 40 Leu Leu Ala Ile Val Phe Ser Leu Asn His Asn Gly Met Pro Val Ile
 245 250 255
 45 Ser Lys Glu Glu Ala Val Asp Met Asp Phe Phe Thr Lys Gln Ile Ile
 260 265 270
 Thr Gly Arg Asp Val His Pro Gly Leu Phe Ala Asn Trp Phe Thr Gly
 275 280 285
 50 Gly Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro Ser Met Pro Arg
 290 295 300
 55 His Asn Phe Ser Lys Ile Gln Pro Ala Val Glu Thr Leu Cys Lys Lys
 305 310 315 320
 Tyr Asn Val Arg Tyr His Thr Thr Gly Met Ile Glu Gly Thr Ala Glu
 325 330 335
 60 Val Phe Ser Arg Leu Asn Glu Val Ser Lys Ala Ala Ser Lys Met Gly
 340 345 350
 Lys Ala Gln
 355

65

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Thr Leu Tyr Thr Leu Ala Phe Val Ala Ala Asn Ser Leu Gly Val
 1 5 10 15
 Leu Tyr Gly Val Leu Ala Cys Pro Ser Val Xaa Pro His Gln Ile Ala
 20 25 30
 Ala Gly Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile Gly Xaa
 35 40 45
 Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Asn Asn Xaa Phe
 50 55 60
 Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ile Ala Trp Trp
 65 70 75 80
 Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp Tyr
 85 90 95
 Gly Pro Asn Leu Gln His Ile Pro
 100

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Val Leu Tyr Gly Val Leu Ala Cys Thr Ser Val Phe Ala His Gln
 1 5 10 15
 Ile Ala Ala Ala Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile
 20 25 30
 Gly His Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Tyr Asn
 35 40 45
 Arg Phe Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ser Ile
 50 55 60
 Ala Trp Trp Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser
 65 70 75 80
 Leu Asp Tyr Asp Pro Asp Leu Gln His Ile Pro Val Phe Ala Val Ser
 85 90 95

5 Thr Lys Phe Phe Ser Ser Leu Thr Ser Arg Phe Tyr Asp Arg Lys Leu
 100 105 110
 10 Thr Phe Gly Pro Val Ala Arg Phe Leu Val Ser Tyr Gln His Phe Thr
 115 120 125
 15 Tyr Tyr Pro Val Asn Cys Phe Gly Arg Ile Asn Leu Phe Ile Gln Thr
 130 135 140
 20 Phe Leu Leu Leu Phe Ser Lys Arg Glu Val Pro Asp Arg Ala Leu Asn
 145 150 155 160
 25 Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro Leu Leu Val Ser
 165 170 175
 30 Cys Leu Pro Asn Trp Pro Glu Arg Phe Phe Phe Val Phe Thr Ser Phe
 180 185 190
 35 Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu Asn His Phe Ala
 195 200 205
 40 Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp Trp Phe Glu Lys
 210 215 220
 45 Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser Tyr Met Asp Trp
 225 230 235 240
 50 Phe Phe Gly Gly Leu Gln Phe Gln Leu Glu His His
 245 250

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

45 Gly Xaa Xaa Asn Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro
 1 5 10 15
 50 Leu Leu Val Ser Cys Leu Pro Asn Trp Pro Glu Arg Phe Xaa Phe Val
 20 25 30
 55 Phe Thr Gly Phe Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu
 35 40 45
 60 Asn His Phe Ala Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp
 50 55 60
 65 Trp Phe Glu Lys Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser
 65 70 75 80
 70 Tyr Met Asp Trp Phe Phe Cys Gly Leu Gln Phe Gln Leu Glu His His
 85 90 95
 75 Leu Phe Pro Arg Leu Pro Arg Cys His Leu Arg Lys Val Ser Pro Val
 100 105 110

Gly Gln Arg Gly Phe Gln Arg Lys Xaa Asn Leu Ser Xaa
 115 120 125

5 (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro Ala Thr Glu Val Gly Gly Leu Ala Trp Met Ile Thr Phe Tyr Val
 1 5 10 15
 Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
 20 25 30
 Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn Trp Phe Val Trp
 35 40 45
 Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
 50 55 60
 Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
 65 70 75 80
 Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
 85 90 95
 His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala
 100 105 110
 Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
 115 120 125
 Lys Pro Leu
 130

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Ser Pro Lys Ser Ser Pro Thr Arg Asn Met Thr Pro Ser Pro Phe
 1 5 10 15
 Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
 20 25 30

5 Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Arg Cys Met Lys Tyr Val
 35 40 45
 Lys Glu Trp Cys Ala Glu Asn Asn Leu Pro Tyr Leu Val Asp Asp Tyr
 50 55 60
 10 Phe Val Gly Tyr Asn Leu Asn Leu Gln Gln Leu Lys Asn Met Ala Glu
 65 70 75 80
 Leu Val Gln Ala Lys Ala Ala
 85

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30 Arg His Glu Ala Ala Arg Gly Gly Thr Arg Leu Ala Tyr Met Leu Val
 1 5 10 15
 Cys Met Gln Trp Thr Asp Leu Leu Trp Ala Ala Ser Phe Tyr Ser Arg
 20 25 30
 35 Phe Phe Leu Ser Tyr Ser Pro Phe Tyr Gly Ala Thr Gly Thr Leu Leu
 35 40 45
 40 Leu Phe Val Ala Val Arg Val Leu Glu Ser His Trp Phe Val Trp Ile
 50 55 60
 Thr Gln Met Asn His Ile Pro Lys Glu Ile Gly His Glu Lys His Arg
 65 70 75 80
 45 Asp Trp Ala Ser Ser Gln Leu Ala Ala Thr Cys Asn Val Glu Pro Ser
 85 90 95
 Leu Phe Ile Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His
 100 105 110
 50 His Leu Phe Pro Thr Met Thr Arg His Asn Tyr Arg Xaa Val Ala Pro
 115 120 125
 55 Leu Val Lys Ala Phe Cys Ala Lys His Gly Leu His Tyr Glu Val
 130 135 140

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5 CCAAGCTTCT GCAGGAGCTC TTTTTTTTTT TTTT 35

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CUACUACUAC UAGGAGTCCT CTACGGTGTT TTG 33

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40 CAUCAUCAUC AUATGATGCT CAAGCTGAAA CTG 33

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: other nucleic acid

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TACCAACTCG AGAAAATGGC TGCTGCTCCC AGTGTGAGG 39

(2) INFORMATION FOR SEQ ID NO:16:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
65 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACTGATCTA GATTACTGCG CCTTACCCAT CTTGGAGGC

39

10 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

25 TACCAACTCG AGAAAATGGC ACCTCCCAAC ACTATCGAT

39

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

40 AACTGATCTA GATTACTTCT TGAAAAAGAC CACGTCTCC

39

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 nucleic acids

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: nucleic acid

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

55 CGTATGTCAC TCCATTCCAA ACTCGTTCAT GGTATCATAA ATATCAACAC ATTTACGCTC 60
 CACTCCTCTA TGGTATTTAC AACTCAAAT ATCGTACTCA AGATTGGGAA GCTTTTGTA 120
 AGGATGGTAA AAATGGTGCA ATTCGTGTTA GTGTCGCCAC AAATTCGAT AAGGCCGCTT 180
 ACGTCATTGG TAAATTGTCT TTGTGTTTCT TCCGTTTCAT CCTTCCACTC CGTTATCATA 240
 GCTTTACAGA TTTAATTTGT TATTTCTCTA TTGCTGAATT CGTCTTTGGT TGGTATCTCA 300
 60 CAATTAATTT CCAAGTTAGT CATGTCGCTG AAGATCTCAA ATTCTTTGCT ACCCCTGAAA 360
 GACCAGATGA ACCATCTCAA ATCAATGAAG ATTGGGCAAT CCTTCAACTT AAAACTACTC 420
 AAGATTATGG TCATGGTTCA CTCCTTTGTA CCTTTTTTAG TGGTTCTTTA AATCATCAAG 480
 TTGTTTCATCA TTTATTCCCA TCAATTGCTC AAGATTCTA CCCACAATT GTACCAATTG 540
 TAAAAGAAGT TTGTAAAGAA CATAACATTA CTTACCACAT TAAACCAAAC TTTACTGAAG 600
 CTATTATGTC ACACATTAAT TACCTTTACA AAATGGGTAA TGATCCAGAT TATGTTAAAA 660
 65 AACCATTAGC CTCAAAGAT GATTAAATGA AATAACTTAA AAACCAATTA TTTACTTTTG 720

ACAAACAGTA ATATTAATAA ATACAA

746

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln
 1 5 10 15
 His Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr
 20 25 30
 Arg Thr Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly
 35 40 45
 Ala Ile Arg Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr
 50 55 60
 Val Ile Gly Lys Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro
 65 70 75
 Leu Arg Tyr His Ser Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile
 80 85 90
 Ala Glu Phe Val Phe Gly Trp Tyr Leu Thr Ile Asn Phe Gln Val
 95 100 105
 Ser His Val Ala Glu Asp Leu Lys Phe Phe Ala Thr Pro Glu Arg
 110 115 120
 Pro Asp Glu Pro Ser Gln Ile Asn Glu Asp Trp Ala Ile Leu Gln
 125 130 135
 Leu Lys Thr Thr Gln Asp Tyr Gly His Gly Ser Leu Leu Cys Thr
 140 145 150
 Phe Phe Ser Gly Ser Leu Asn His Gln Val Val His His Leu Phe
 155 160 165
 Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu Val Pro Ile Val
 170 175 180
 Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His Ile Lys Pro
 185 190 195
 Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu Tyr Lys
 200 205 210
 Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser Lys
 215 220 225
 Asp Asp ***

(2) INFORMATION FOR SEQ ID NO 21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 494 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTGGAAGG NTCCAAGTTN ACCACGGANT NGGCAAGTTN ACGGGGCGGA AANCGGTTTT 60
 CCCCCAAGC CTTTGTGCGA CTGGTCTGT GGTGGCTTCC AGTACCAAGT CGACCACCAC 120
 TTATCCCCA GCCTGCCCGG ACACAATCTG GCCAAGACAC ACGCACTGGT CGAATCGTTC 180
 TGCAAGGAGT GGGGTGTCCA GTACCACGAA GCCGACCTCG TGGACGGGAC CATGGAAGTC 240
 TTGCACCATT TGGGCAGCGT GGCCGGCGAA TTCGTCGTGG ATTTTGTACG CGACGGACCC 300

GCCATGTAAT CGTCGTTCGT GACGATGCAA GGGTTCACGC ACATCTACAC ACACTCACTC 360
 ACACAAC TAGTAACTCGT ATAGAATTCG GTGTGACCT GGACCTTGTT TGACTGGTTG 420
 GGGATAGGGT AGGTAGGCGG ACGCGTGGGT CGNCCCCGGG AATTCTGTGA CCGGTACCTG 480
 GCGCGCTNA AAGT 494

5

(2) INFORMATION FOR SEQ ID NO:22:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

20

Phe Trp Lys Xxx Pro Ser Xxx Pro Arg Xxx Xxx Gln Val Xxx Gly
 1 5 10 15
 Ala Glu Xxx Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys
 20 25 30
 Gly Gly Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu
 25 35 40 45
 Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe
 50 55 60
 Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp
 65 70 75
 Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly Glu
 30 65 70 75
 Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met
 80 85

35

40

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 nucleic acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: nucleic acid

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCGACGTG GTTAAAGCGT CATGGGTGCG 60
 CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTACTTGT GCGCCTTTGG TCTCGGCTGC 120
 ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACCCATT TGCCCGTGAG CAACCCGGAG 180
 GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCACACTGT GAACATCAGC ACCAAGTCGT 240
 GGTTCGTCAC ATGGTGGATG TCGAACCTCA ACTTTCAGAT CGAGCACCAC CTTTTCCCA 300
 CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCGCGCGT CGAGGCCCTC TTCAAGCGCC 360
 ACGGTCTCCC TTACTACGAC ATGCCCTACA CGAGCGCCGT CTCCACCACC TTTGCCAACC 420
 TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAGCGCGA CTAGCCTCTT TTCCTAGACC 480
 TTAATTCCCC ACCCCACCCC ATGTTCTGTC TTCTCCCGC 520

60

(2) INFORMATION FOR SEQ ID NO:24:

65

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

10

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Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys
1      5      10      15
Arg His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His
20      25      30
Val Leu Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala
35      40      45
Val Arg Arg Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly
50      55      60
Ser Ala Ala Leu Ala Arg Val Arg Ala Asp His Thr Val Asn Ile
20      65      70      75
Ser Thr Lys Ser Trp Phe Val Thr Trp Trp Met Ser Asn Leu Asn
80      85      90
Phe Gln Ile Glu His His Leu Phe Pro Thr Ala Pro Gln Phe Arg
95      100      105
25      Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu Phe Lys Arg His
110      115      120
Gly Leu Pro Tyr Tyr Asp Met Pro Tyr Thr Ser Ala Val Ser Thr
125      130      135
30      Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly Asp Ala
140      145      150
Lys Arg Asp

```

35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: nucleic acid

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

ACGCGTCCGC CCACGCGTCC GCCGCGAGCA ACTCATCAAG GAAGGCTACT TTGACCCCTC 60
GCTCCCGCAC ATGACGTACC GCGTGGTCGA GATTGTTGTT CTCTTCGTGC TTTCCTTTTG 120
GCTGATGGGT CAGTCTTCAC CCCTCGCGCT CGCTCTCGGC ATTGTCGTCA GCGGCATCTC 180
TCAGGGTCGC TCGGCTGGG TAATGCATGA GATGGGCCAT GGGTCGTCA CTGGTGTCAT 240
TTGGCTTGAC GACCGTTGT GCGAGTTCTT TTACGGCGTT GGTGTGGCA TGAGCGGTCA 300
TTACTGGAAG AACGAGCACA GCAAACACCA CGCAGCGCCA AACCGGCTCG AGCAGGATGT 360
AGATCTCAAC ACCTTGCCAT TGGTGGCCTT CAACGAGCGC GTCGTGCGCA AGGTCCGACC 420

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55

(2) INFORMATION FOR SEQ ID NO:26:

60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

65

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

5 Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly
 1 5 10 15
 Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu
 20 30
 10 Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser
 35 40 45
 Ser Pro Leu Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser
 50 55 60
 Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser
 65 70 75
 15 Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe
 65 70 75
 Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln
 80 85 90
 20 His Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val
 95 100 105
 Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val
 110 115 120
 Arg Lys Val Arg Pro
 125

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2692004)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

40 GCACGCCGAC CGGCGCCGGG AGATCCTGGC AAAGTATCCA GAGATAAAGT CCTTGATGAA 60
 ACCTGATCCC AATTTGATAT GGATTATAAT TATGATGGTT CTCACCCAGT TGGGTGCATT 120
 45 TTACATAGTA AAAGACTTGG ACTGGAAATG GGTCAATTTT GGGGCCTATG CGTTTGGCAG 180
 TTGCATTAAC CACTCAATGA CTCTGGCTAT TCATGAGATT GCCCACAATG CTGCCTTTGG 240
 CAACTGCAAA GCAATGTGGA ATCGCTGGTT TGGAATGTTT GCTAATCTTC CTATTGGGAT 300
 50 TCCATATTCA ATTTCTTTTA AGAGGTATCA CATGGATCAT CATCGGTACC TTGGAGCTGA 360
 TGGCGTCGAT GTAGATATTC CTACCGATTT TGAGGGCTGG TTCTTCTGTA CCGCTTTCAG 420
 55 AAAGTTTATA TGGGTTATTC TTCAGCCTCT CTTTTATGCC TTTCGACCTC TGTTTCATCA 480
 CCCCAAACCA ATTACGTATC TGGAAGTTAT CAATACCGTG GCACAGGTCA CTTTTGACAT 540
 TTTAATTTAT TACTTTTTGG GAATTAAATC CTTAGTCTAC ATGTTGGCAG CATCTTTACT 600
 60 TGGCCTGGGT TTGCACCCAA TTTCTGGACA TTTTATAGCT GAGCATTACA TGTTCTTAAA 660
 GGGTCATGAA ACTTACTCAT ATTATGGGCC TCTGAATTTA CTTACCTTCA ATGTGGGTTA 720
 TCATAATGAA CATCATGATT TCCCCAACAT TCCTGGAAAA AGTCTTCCAC TGGTGAGGAA 780
 65 AATAGCAGCT GAATACTATG ACAACCTCCC TCACTACAA TCCCTGGATAA AAGTACTGTA 840

5 TGATTTTGTG ATGGATGATA CAATAAGTCC CTAACAAGA ATGAAGAGGC ACCAAAAAGG 900
 AGAGATGGTG CTGGAGTAAA TATCATTAGT GCCAAAGGGA TTCTTCTCCA AAACCTTAGA 960
 TGATAAAATG GAATTTTTCG ATTATTAAAC TTGAGACCAG TGATGCTCAG AAGCTCCCCT 1020
 GGCACAATTT CAGAGTAAGA GCTCGGTGAT ACCAAGAAGT GAATCTGGCT TTAAACAGT 1080
 10 CAGCCTGACT CTGTACTGCT CAGTTTCACT CACAGGAAAC TTGTGACTTG TGTATTATCG 1140
 TCATTGAGGA TGTTTCACTC ATGTCTGTCA TTTTATAAGC ATATCATTTA AAAAGCTTCT 1200
 15 AAAAAGCTAT TTCGCCAGG 1219

(2) INFORMATION FOR SEQ ID NO:28:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2153526)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

30 TTACCTTCTA CGTCCGCTTC TTCCTCACTT ATGTGCCACT ATTGGGGCTG AAAGCTTCCT 60
 GGGCCTTTTC TTCATAGTCA GGTTCTGGA AAGCAACTGG TTTGTGTGGG TGACACAGAT 120
 35 GAACCATATT CCCATGCACA TTGATCATGA CCGGAACATG GACTGGGTTT CCACCCAGCT 180
 CCAGGCCACA TGCAATGTCC ACAAGTCTGC CTTCAATGAC TGGTTCAGTG GACACCTCAA 240
 40 CTTCCAGATT GAGCACCATC TTTTCCAC GATGCCTCGA CACAATTACC ACAAAGTGGC 300
 TCCCCTGGTG CAGTCCTTGT GTGCCAAGCA TGGCATAGAG TACCAGTCCA AGCCCCTGCT 360
 GTCAGCCTTC GCCGACATCA TCCACTCACT AAAGGAGTCA GGGCAGCTCT GGCTAGATGC 420
 45 CTATCTTAC CAATAACAAC AGCCACCCTG CCCAGTCTGG AAGAAGAGGA GGAAGACTCT 480
 GGAGCCAAGG CAGAGGGGAG CTTGAGGGAC AATGCCACTA TAGTTTAATA CTCAGAGGGG 540
 50 GTTGGGTTTG GGGACATAAA GCCTCTGACT CAAACTCCTC CCTTTTATCT TCTAGCCACA 600
 GTTCTAAGAC CCAAAGTGGG GGGTGGACAC AGAAGTCCCT AGGAGGGAAG GAGCT 655

(2) INFORMATION FOR SEQ ID NO:29:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3506132)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

65 GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTGT CCTTGCTACC 60

5 TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120
 CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180
 AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240
 10 CCCGATGTGA ACATGCTGCA CGTGTGTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300
 AAGA 304

(2) INFORMATION FOR SEQ ID NO:30:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 918 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

25 CAGGGACCTA CCCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG 60
 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 30 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCGAG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CCTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 35 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGGTC 420
 TTTGGGACGT CCTTTTTGCC CTTCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGGCC 480
 40 CAGGCTGGCT GGCTGCAGCA TGACTTTGGG CACCTGTCGG TCTTCAGCAC CTCAAAGTGG 540
 AACCATCTGC TACATCATTT TGTGATTGGC CACCTGAAGG GGGCCCCCGC CAGTTGGTGG 600
 45 AACCACATGC ACTTCCAGCA CCATGCCAAG CCCAACTGCT TCCGCAAAGA CCCAGACATC 660
 AACATGCATC CCTTCTTCTT TGCCTTGGGG AAGATCCTCT CTGTGGAGCT TGGGAAACAG 720
 50 AAGAAAAAAT ATATGCCGTA CAACCACCAG CACARATACT TCTTCCTAAT TGGGCCCCCA 780
 GCCTTGCTGC CTCTCTACTT CCAGTGGTAT ATTTTCTATT TTGTTATCCA GCGAAAGAAG 840
 TGGGTGGACT TGGCCTGGAT CAGCAAACAG GAATACGATG AAGCCGGGCT TCCATTGTCC 900
 55 ACCGCAAATG CTTCTAAA 918

(2) INFORMATION FOR SEQ ID NO:31:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1686 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 65 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2511785)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | | |
|----|--|------|
| 5 | GCCACTTAAA GGGTGCCTCT GCCAACTGGT GGAATCATCG CCACTTCCAG CACCACGCCA | 60 |
| | AGCCTAACAT CTTCCACAAG GATCCCGATG TGAACATGCT GCACGTGTTT GTTCTGGGCG | 120 |
| 10 | AATGGCAGCC CATCGAGTAC GGCAAGAAGA AGCTGAAATA CCTGCCCTAC AATCACCAGC | 180 |
| | ACGAATACTT CTTCTGATT GGGCCGCCGC TGCTCATCCC CATGTATTTT CAGTACCAGA | 240 |
| | TCATCATGAC CATGATCGTC CATAAGAACT GGGTGGACCT GGCCTGGGCC GTCAGCTACT | 300 |
| 15 | ACATCCGGTT CTTTCATCACC TACATCCCTT TCTACGGCAT CCTGGGAGCC CTCCTTTTCC | 360 |
| | TCAACTTCAT CAGGTTCTTG GAGAGCCACT GGTTTGTGTG GGTCACACAG ATGAATCACA | 420 |
| 20 | TCGTCATGGA GATTGACCAG GAGGCCTACC GTGACTGGTT CAGTAGCCAG CTGACAGCCA | 480 |
| | CCTGCAACGT GGAGCAGTCC TTCTTCAACG ACTGGTTCAG TGGACACCTT AACTTCCAGA | 540 |
| | TTGAGCACCA CCTCTTCCCC ACCATGCCCC GGCACAACTT ACACAAGATC GCCCCGCTGG | 600 |
| 25 | TGAAGTCTCT ATGTGCCAAG CATGGCATTG AATACCAGGA GAAGCCGCTA CTGAGGGCCC | 660 |
| | TGCTGGACAT CATCAGGTCC CTGAAGAAGT CTGGGAAGCT GTGGCTGGAC GCCTACCTTC | 720 |
| 30 | ACAAATGAAG CCACAGCCCC CGGGACACCG TGGGAAGGG GTGCAGGTGG GGTGATGGCC | 780 |
| | AGAGGAATGA TGGGCTTTTG TTCTGAGGGG TGTCCGAGAG GCTGGTGTAT GCACTGCTCA | 840 |
| | CGGACCCCAT GTTGGATCTT TCTCCCTTTC TCCTCTCCTT TTTCTCTTCA CATCTCCCCC | 900 |
| 35 | ATAGCACCTT GCCCTCATGG GAQCTGCCCT CCCTCAGCCG TCAGCCATCA GCCATGGCCC | 960 |
| | TCCAGTGCC TCCTAGCCCC TTCTTCCAAG GAGCAGAGAG GTGGCCACCG GGGGTGGCTC | 1020 |
| 40 | TGTCCTACCT CCACTCTCTG CCCCTAAAGA TGGGAGGAGA CCAGCGGTCC ATGGGTCTGG | 1080 |
| | CCTGTGAGTC TCCCTTGCA GCCTGGTCAC TAGGCATCAC CCCCCTTTG GTTCTTCAGA | 1140 |
| | TGCTCTTGGG GTTCATAGGG GCAGGTCCTA GTCGGGCAGG GCCCCTGACC CTCCCGGCT | 1200 |
| 45 | GGCTTCACTC TCCCTGACGG CTGCCATTGG TCCACCCTTT CATAGAGAGG CCTGCTTTGT | 1260 |
| | TACAAAGCTC GGGTCTCCCT CCTGCAGCTC GGTTAAGTAC CCGAGGCCTC TCTTAAGATG | 1320 |
| 50 | TCCAGGGCCC CAGGCCCGCG GGCACAGCCA GCCCAAACCT TGGGCCCTGG AAGAGTCCTC | 1380 |
| | CACCCCATCA CTAGAGTGCT CTGACCCTGG GCTTTCACGG GCCCCATTCC ACCGCCTCCC | 1440 |
| | CAACTTGAGC CTGTGACCTT GGGACCAAAG GGGGAGTCCC TCGTCTCTTG TGA CTGAGCA | 1500 |
| 55 | GAGGCAGTGG CCACGTTGAG GGAGGGGCCG GCTGGCCTGG AGGCTCAGCC CACCCTCCAG | 1560 |
| | CTTTTCCTCA GGGTGTCTTG AGGTCCAAGA TTCTGGAGCA ATCTGACCCT TCTCCAAAGG | 1620 |
| 60 | CTCTGTTATC AGCTGGGCAG TGCCAGCCAA TCCCTGGCCA TTTGGCCCCA GGGGACGTGG | 1680 |
| | GCCCTG | 1686 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1843 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid (Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

10

GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC 60

TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120

15

CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180

AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240

20

CCCGATGTGA ACATGCTGCA CGTGTGTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300

AAGAAGAAGC TGAAATACCT GCCCTACAAT CACCAGCACG AATACTTCTT CCTGATTGGG 360

CCGCCGCTGC TCATCCCCAT GTATTTCCAG TACCAGATCA TCATGACCAT GATCGTCCAT 420

25

AAGAACTGGG TGGACCTGGC CTGGGCCGTC AGCTACTACA TCCGGTTCTT CATCACCTAC 480

ATCCCTTTCT ACGGCATCCT GGGAGCCCTC CTTTTCTCA ACTTCATCAG GTTCCTGGAG 540

30

AGCCACTGGT TTGTGTGGGT CACACAGATG AATCACATCG TCATGGAGAT TGACCAGGAG 600

GCCTACCGTG ACTGGTTCAG TAGCCAGCTG ACAGCCACCT GCAACGTGGA GCAGTCCTTC 660

TTCAACGACT GGTTCAGTGG ACACCTTAAC TTCCAGATTG AGCACCACCT CTTCCCCACC 720

35

ATGCCCCGGC ACAACTTACA CAAGATCGCC CCGCTGGTGA AGTCTCTATG TGCCAAGCAT 780

GGCATTGAAT ACCAGGAGAA GCCGCTACTG AGGGCCCTGC TGGACATCAT CAGGTCCCTG 840

40

AAGAAGTCTG GGAAGCTGTG GCTGGACGCC TACCTTCACA AATGAAGCCA CAGCCCCCGG 900

GACACCGTGG GGAAGGGGTG CAGGTGGGGT GATGGCCAGA GGAATGATGG GCTTTTGTTC 960

TGAGGGGTGT CCGAGAGGCT GGTGTATGCA CTGCTCACGG ACCCATGTT GGATCTTTCT 1020

45

CCCTTTCTCC TCTCCTTTT CTCTTCACAT CTCCTCCATA GCACCCTGCC CTCATGGGAC 1080

CTGCCCTCCC TCAGCCGTCA GCCATCAGCC ATGGCCCTCC CAGTGCCTCC TAGCCCTTC 1140

50

TTCCAAGGAG CAGAGAGGTG GCCACCGGGG GTGGCTCTGT CCTACCTCCA CTCTCTGCCC 1200

CTAAAGATGG GAGGAGACCA GCGGTCCATG GGTCTGGCCT GTGAGTCTCC CTTGCAGCC 1260

TGGTCACTAG GCATCACCCC CGCTTTGGTT CTTCAGATGC TCTTGGGGTT CATAGGGGCA 1320

55

GGTCCTAGTC GGGCAGGGCC CCTGACCCTC CCGGCCTGGC TTCACTCTCC CTGACGGCTG 1380

CCATTGGTCC ACCCTTTCAT AGAGAGGCCT GCTTTGTAC AAAGCTCGGG TCTCCCTCCT 1440

60

GCAGCTCGGT TAAGTACCCG AGGCCTCTCT TAAGATGTCC AGGGCCCCAG GCGCGGGG 1500

ACAGCCAGCC CAAACCTTGG GCCCTGGAAG AGTCCTCCAC CCCATCACTA GAGTGCTCTG 1560

ACCCTGGGCT TTCACGGGCC CCATTCCACC GCCTCCCCAA CTTGAGCCTG TGACCTTGGG 1620

65

ACCAAAGGGG GAGTCCCTCG TCTCTTGTA CTCAGCAGAG GCAGTGCCA CGTTCAGGGA 1680

GGGGCCGGCT GGCCTGGAGG CTCAGCCCAC CCTCCAGCTT TTCCTCAGGG TGTCTGAGG 1740
 TCCAAGATTC TGGAGCAATC TGACCCTTCT CCAAAGGCTC TGTTATCAGC TGGGCAGTGC 1800
 5 CAGCCAATCC CTGGCCATTT GGCCCCAGGG GACGTGGGCC CTG 1843

(2) INFORMATION FOR SEQ ID NO:33:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 253538a)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

20 CAGGGACCTA CCCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG 60
 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 25 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CCTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 30 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGGTC 420
 TTTGGGACGT CTTTTTTGCC CTTCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGCAG 480
 35 GCCCAAGCTG GATGGCTGCA ACATGATTAT GGCCACCTGT CTGTCTACAG AAAACCCAAG 540
 TGGAACCACC TTGTCCACAA ATTCGTCATT GGCCACTTAA AGGGTGCCTC TGCCAACCTGG 600
 40 TGGAATCATC GCCACTTCCA GCACCACGCC AAGCCTAACA TCTTCCACAA GGATCCCGAT 660
 GTGAACATGC TGCACGTGTT TGTCTGGGGC GAATGGCAGC CCATCGAGTA CGGCAAGAAG 720
 AAGCTGAAAT ACCTGCCCTA CAATCACCAG CACGAATACT TCTTCTGAT TGGGCCGCCG 780
 45 CTGCTCATCC CCATGTATTT CCAGTACCAG ATCATCATGA CCATGATCGT CCATAAGAAC 840
 TGGGTGGACC TGGCCTGGGC CGTCAGCTAC TACATCCGGT TCTTCATCAC CTACATCCCT 900
 50 TTCTACGGCA TCCTGGGAGC CCTCCTTTTC CTCAACTTCA TCAGGTTCCCT GGAGAGCCAC 960
 TGGTTTGTGT GGGTCACACA GATGAATCAC ATCGTCATGG AGATTGACCA GGAGGCCTAC 1020
 55 CGTGACTGGT TCAGTAGCCA GCTGACAGCC ACCTGCAACG TGGAGCAGTC CTTCTTCAAC 1080
 GACTGGTTCA GTGGACACCT TAACTTCCAG ATTGAGCACC ACCTCTTCCC CACCATGCCC 1140
 CGGCACAACT TACACAAGAT CGCCCCGCTG GTGAAGTCTC TATGTGCCAA GCATGGCATT 1200
 60 GAATACCAGG AGAAGCCGCT ACTGAGGGCC CTGCTGGACA TCATCAGGTC CCTGAAGAAG 1260
 TCTGGGAAGC TGTGGCTGGA CGCCTACCTT CACAAATGAA GCCACAGCCC CCGGGACACC 1320
 GTGGGGAAGG GGTGCAGGTG GGGTGATGGC CAGAGGAATG ATGGGCTTTT GTTCTGAGGG 1380
 65 GTGTCCGAGA GGCTGGTGTA TGCACTGCTC ACGGACCCCA TGTGGATCT TTCTCCCTTT 1440

CTCCTCTCCT TTTTCTCTTC ACATCTCCCC CATAGCACCC TGCCCTCATG GGACCTGCCC 1500
 5 TCCCTCAGCC GTCAGCCATC AGCCATGGCC CTCCCAGTGC CTCCTAGCCC CTTCTTCCAA 1560
 GGAGCAGAGA GGTGGCCACC GGGGGTGGCT CTGTCTTACC TCCACTCTCT GCCCCTAAAG 1620
 ATGGGAGGAG ACCAGCGGTC CATGGGTCTG GCCTGTGAGT CTCCCCTTGC AGCCTGGTCA 1680
 10 CTAGGCATCA CCCCCGCTTT GTTCTTTCAG ATGCTCTTGG GGTTCATAGG GGCAGGTCCT 1740
 AGTCGGGCAG GGGCCCTGAC CCTCCCGGCC TGGCTTCACT CTCCCTGACG GCTGCCATTG 1800
 15 GTCCACCCTT TCATAGAGAG GCCTGCTTTG TTACAAAGCT CGGGTCTCCC TCCTGCAGCT 1860
 CGGTAAAGTA CCCGAGGCCT CTCTTAAGAT GTCCAGGGCC CCAGGCCCCG GGGCACAGCC 1920
 AGCCCAAACC TTGGGCCCTG GAAGAGTCCT CCACCCCATC ACTAGAGTGC TCTGACCCTG 1980
 20 GGCTTTCACG GGGCCCATTC CACCGCTCC CCAACTTGAG CCTGTGACCT TGGGACCAAA 2040
 GGGGGAGTCC CTCGTCTCTT GTGACTCAGC AGAGGCAGTG GCCACGTTCA GGGAGGGGCC 2100
 25 GGCTGGCCTG GAGGCTCAGC CCACCCTCCA GCTTTTCCTC AGGGTGTCTT GAGGTCCAAG 2160
 ATTCTGGAGC AATCTGACCC TTCTCAAAG GCTCTGTTAT CAGCTGGGCA GTGCCAGCCA 2220
 ATCCCTGGCC ATTGGCCCC AGGGGACGTG GGCCCTG 2257

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

45 His Ala Asp Arg Arg Arg Glu Ile Leu Ala Lys Tyr Pro Glu Ile
 1 5 10 15
 Lys Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile
 20 25 30
 50 Met Met Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp
 35 40 45
 Leu Asp Trp Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser
 50 55 60
 Cys Ile Asn His Ser Met Thr Leu Ala Ile His Glu Ile Ala His
 65 70 75
 55 Asn Ala Ala Phe Gly Asn Cys Lys Ala Met Trp Asn Arg Trp Phe
 80 85 90
 Gly Met Phe Ala Asn Leu Pro Ile Gly Ile Pro Tyr Ser Ile Ser
 95 100 105
 Phe Lys Arg Tyr His Met Asp His His Arg Tyr Leu Gly Ala Asp
 110 115 120
 60 Gly Val Asp Val Asp Ile Pro Thr Asp Phe Glu Gly Trp Phe Phe
 125 130 135
 Cys Thr Ala Phe Arg Lys Phe Ile Trp Val Ile Leu Gln Pro Leu
 140 145 150
 65 Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn Pro Lys Pro Ile Thr
 155 160 165
 Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val Thr Phe Asp Ile

5 Leu Ile Tyr Tyr 170 Phe Leu Gly Ile Lys Ser Leu Val Tyr Met Leu
 185 190 195
 Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser Gly His
 200 205 210
 Phe Ile Ala Glu His Tyr Met Phe Leu Lys Gly His Glu Thr Tyr
 215 220 225
 Ser Tyr Tyr Gly Pro Leu Asn Leu Leu Thr Phe Asn Val Gly Tyr
 230 235 240
 10 His Asn Glu His His Asp Phe Pro Asn Ile Pro Gly Lys Ser Leu
 245 250 255
 Pro Leu Val Arg Lys Ile Ala Ala Glu Tyr Tyr Asp Asn Leu Pro
 260 265 270
 15 His Tyr Asn Ser Trp Ile Lys Val Leu Tyr Asp Phe Val Met Asp
 275 280 285
 Asp Thr Ile Ser Pro Tyr Ser Arg Met Lys Arg His Gln Lys Gly
 290 295 300
 Glu Met Val Leu Glu *** Ile Ser Leu Val Pro Lys Gly Phe Phe
 305 310 315
 20 Ser Lys Thr Leu Asp Asp Lys Met Glu Phe Leu His Tyr *** Thr
 320 325 330
 *** Asp Gln *** Cys Ser Glu Ala Pro Leu Ala Gln Phe Gln Ser
 335 340 345
 25 Lys Ser Ser Val Ile Pro Arg Ser Glu Ser Gly Phe *** Thr Val
 350 355 360
 Ser Leu Thr Leu Tyr Cys Ser Val Ser Leu Thr Gly Asn Leu ***
 365 370 375
 30 Leu Val Tyr Tyr Arg His *** Gly Cys Phe Thr His Val Cys His
 380 385 390
 Phe Ile Ser Ile Ser Phe Lys Lys Leu Leu Lys Ser Tyr Phe Ala
 400 405 410
 Arg

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2153526)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Tyr Leu Leu Arg Pro Leu Leu Pro His Leu Cys Ala Thr Ile Gly
 1 5 10 15
 50 Ala Glu Ser Phe Leu Gly Leu Phe Phe Ile Val Arg Phe Leu Glu
 20 25 30
 Ser Asn Trp Phe Val Trp Val Thr Gln Met Asn His Ile Pro Met
 35 40 45
 His Ile Asp His Asp Arg Asn Met Asp Trp Val Ser Thr Gln Leu
 50 55 60
 55 Gln Ala Thr Cys Asn Val His Lys Ser Ala Phe Asn Asp Trp Phe
 65 70 75
 Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
 80 85 90
 60 Met Pro Arg His Asn Tyr His Lys Val Ala Pro Leu Val Gln Ser
 95 100 105
 Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser Lys Pro Leu Leu
 110 115 120
 Ser Ala Phe Ala Asp Ile Ile His Ser Leu Lys Glu S r Gly Gln
 125 130 135
 65 Leu Trp Leu Asp Ala Tyr Leu His Gln *** Gln Gln Pro Pro Cys
 140 145 150

5 Pro Val Trp Lys Lys Arg Arg Lys Thr Leu Glu Pro Arg Gln Arg
 155 160 165
 Gly Ala *** Gly Thr Met Pro Leu *** Phe Asn Thr Gln Arg Gly
 170 175 180
 10 Leu Gly Leu Gly Thr *** Ser Leu *** Leu Lys Leu Leu Pro Phe
 185 190 195
 Ile Phe *** Pro Gln Phe *** Asp Pro Lys Trp Gly Val Asp Thr
 200 205 210
 15 Glu Val Pro Arg Arg Glu Gly Ala
 215

15 (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

30 Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
 1 5 10 15
 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
 20 25 30
 Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
 35 35 40 45
 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
 50 55 60
 Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
 65 70 75
 40 Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xxx
 80 85

45 (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 amino acids
 (B) TYPE: amino acid
 50 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3854933)

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

60 Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
 1 5 10 15
 Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
 20 25 30
 Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
 35 40 45
 Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
 50 55 60
 65 Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
 65 70 75
 Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro

5 80 85 90
 Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
 95 100 105
 Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
 110 115 120
 Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
 125 130 135
 Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
 140 145 150
 10 Cys Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp Leu
 155 160 165
 Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp
 170 175 180
 15 Asn His Leu Leu His His Phe Val Ile Gly His Leu Lys Gly Ala
 185 190 195
 Pro Ala Ser Trp Trp Asn His Met His Phe Gln His His Ala Lys
 200 205 210
 Pro Asn Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro Phe
 215 220 225
 20 Phe Phe Ala Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln
 230 235 240
 Lys Lys Lys Tyr Met Pro Tyr Asn His Gln His Xxx Tyr Phe Phe
 245 250 255
 25 Leu Ile Gly Pro Pro Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr
 260 265 270
 Ile Phe Tyr Phe Val Ile Gln Arg Lys Lys Trp Val Asp Leu Ala
 275 280 285
 Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly Leu Pro Leu Ser
 290 295 300
 30 Thr Ala Asn Ala Ser Lys
 305

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

50 5 10 15
 His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe
 20 25 30
 Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val
 35 40 45
 Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu
 50 55 60
 Tyr Gly Lys Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His
 65 70 75
 55 Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr
 80 85 90
 Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp
 95 100 105
 60 Val Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile
 110 115 120
 Thr Tyr Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu
 125 130 135
 Asn Phe Ile Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr
 140 145 150
 65 Gln Met Asn His Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg

Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln
 155 160 165
 Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile
 170 175 180
 Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu His Lys
 185 190 195
 Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu
 200 205 210
 Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg
 215 220 225
 Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His
 230 235 240
 Lys *** Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg
 245 250 255
 Trp Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe *** Gly Val
 260 265 270
 Ser Glu Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp
 275 280 285
 Leu Ser Pro Phe Leu Leu Ser Phe Phe Ser Ser His Leu Pro His
 290 295 300
 Ser Thr Leu Pro Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro
 305 310 315
 Ser Ala Met Ala Leu Pro Val Pro Pro Ser Pro Phe Phe Gln Gly
 320 325 330
 Ala Glu Arg Trp Pro Pro Gly Val Ala Leu Ser Tyr Leu His Ser
 335 340 345
 Leu Pro Leu Lys Met Gly Gly Asp Gln Arg Ser Met Gly Leu Ala
 350 355 360
 Cys Glu Ser Pro Leu Ala Ala Trp Ser Leu Gly Ile Thr Pro Ala
 365 370 375
 Leu Val Leu Gln Met Leu Leu Gly Phe Ile Gly Ala Gly Pro Ser
 380 385 390
 Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp Leu His Ser Pro ***
 400 405 410
 Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg Pro Ala Leu Leu
 415 420 425
 Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser Thr Arg Gly
 430 435 440
 Leu Ser *** Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala Ser
 445 450 455
 Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His *** Ser
 460 465 470
 Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro
 475 480 485
 Thr *** Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu
 490 495 500
 Leu *** Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly
 505 510 515
 Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val
 520 525 530
 Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala
 535 540 545
 Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala
 550 555 560
 Pro Gly Asp Val Gly Pro Xxx
 565

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 619 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Tyr | Phe | Gly | Asn | Gly | Trp | Ile | Pro | Thr | Leu | Ile | Thr | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |
| Phe | Val | Leu | Ala | Thr | Ser | Gln | Ala | Gln | Ala | Gly | Trp | Leu | Gln | His |
| | | | | 20 | | | | | 25 | | | | | 30 |
| Asp | Tyr | Gly | His | Leu | Ser | Val | Tyr | Arg | Lys | Pro | Lys | Trp | Asn | His |
| | | | | 35 | | | | | 40 | | | | | 45 |
| Leu | Val | His | Lys | Phe | Val | Ile | Gly | His | Leu | Lys | Gly | Ala | Ser | Ala |
| | | | | 50 | | | | | 55 | | | | | 60 |
| Asn | Trp | Trp | Asn | His | Arg | His | Phe | Gln | His | His | Ala | Lys | Pro | Asn |
| | | | | 65 | | | | | 70 | | | | | 75 |
| Ile | Phe | His | Lys | Asp | Pro | Asp | Val | Asn | Met | Leu | His | Val | Phe | Val |
| | | | | 80 | | | | | 85 | | | | | 90 |
| Leu | Gly | Glu | Trp | Gln | Pro | Ile | Glu | Tyr | Gly | Lys | Lys | Lys | Leu | Lys |
| | | | | 95 | | | | | 100 | | | | | 105 |
| Tyr | Leu | Pro | Tyr | Asn | His | Gln | His | Glu | Tyr | Phe | Phe | Leu | Ile | Gly |
| | | | | 110 | | | | | 115 | | | | | 120 |
| Pro | Pro | Leu | Leu | Ile | Pro | Met | Tyr | Phe | Gln | Tyr | Gln | Ile | Ile | Met |
| | | | | 125 | | | | | 130 | | | | | 135 |
| Thr | Met | Ile | Val | His | Lys | Asn | Trp | Val | Asp | Leu | Ala | Trp | Ala | Val |
| | | | | 140 | | | | | 145 | | | | | 150 |
| Ser | Tyr | Tyr | Ile | Arg | Phe | Phe | Ile | Thr | Tyr | Ile | Pro | Phe | Tyr | Gly |
| | | | | 155 | | | | | 160 | | | | | 165 |
| Ile | Leu | Gly | Ala | Leu | Leu | Phe | Leu | Asn | Phe | Ile | Arg | Phe | Leu | Glu |
| | | | | 170 | | | | | 175 | | | | | 180 |
| Ser | His | Trp | Phe | Val | Trp | Val | Thr | Gln | Met | Asn | His | Ile | Val | Met |
| | | | | 185 | | | | | 190 | | | | | 195 |
| Glu | Ile | Asp | Gln | Glu | Ala | Tyr | Arg | Asp | Trp | Phe | Ser | Ser | Gln | Leu |
| | | | | 200 | | | | | 205 | | | | | 210 |
| Thr | Ala | Thr | Cys | Asn | Val | Glu | Gln | Ser | Phe | Phe | Asn | Asp | Trp | Phe |
| | | | | 215 | | | | | 220 | | | | | 225 |
| Ser | Gly | His | Leu | Asn | Phe | Gln | Ile | Glu | His | His | Leu | Phe | Pro | Thr |
| | | | | 230 | | | | | 235 | | | | | 240 |
| Met | Pro | Arg | His | Asn | Leu | His | Lys | Ile | Ala | Pro | Leu | Val | Lys | Ser |
| | | | | 245 | | | | | 250 | | | | | 255 |
| Leu | Cys | Ala | Lys | His | Gly | Ile | Glu | Tyr | Gln | Glu | Lys | Pro | Leu | Leu |
| | | | | 260 | | | | | 265 | | | | | 270 |
| Arg | Ala | Leu | Leu | Asp | Ile | Ile | Arg | Ser | Leu | Lys | Lys | Ser | Gly | Lys |
| | | | | 275 | | | | | 280 | | | | | 285 |
| Leu | Trp | Leu | Asp | Ala | Tyr | Leu | His | Lys | *** | Ser | His | Ser | Pro | Arg |
| | | | | 290 | | | | | 295 | | | | | 300 |
| Asp | Thr | Val | Gly | Lys | Gly | Cys | Arg | Trp | Gly | Asp | Gly | Gln | Arg | Asn |
| | | | | 305 | | | | | 310 | | | | | 315 |
| Asp | Gly | Leu | Leu | Phe | *** | Gly | Val | Ser | Glu | Arg | Leu | Val | Tyr | Ala |
| | | | | 320 | | | | | 325 | | | | | 330 |
| Leu | Leu | Thr | Asp | Pro | Met | Leu | Asp | Leu | Ser | Pro | Phe | Leu | Leu | Ser |
| | | | | 335 | | | | | 340 | | | | | 345 |
| Phe | Phe | Ser | Ser | His | Leu | Pro | His | Ser | Thr | Leu | Pro | Ser | Trp | Asp |
| | | | | 350 | | | | | 355 | | | | | 360 |
| Leu | Pro | Ser | Leu | Ser | Arg | Gln | Pro | Ser | Ala | Met | Ala | Leu | Pro | Val |
| | | | | 365 | | | | | 370 | | | | | 375 |
| Pro | Pro | Ser | Pro | Phe | Phe | Gln | Gly | Ala | Glu | Arg | Trp | Pro | Pro | Gly |
| | | | | 380 | | | | | 385 | | | | | 390 |
| Val | Ala | Leu | Ser | Tyr | Leu | His | Ser | Leu | Pro | Leu | Lys | Met | Gly | Gly |
| | | | | 400 | | | | | 405 | | | | | 410 |
| Asp | Gln | Arg | Ser | Met | Gly | Leu | Ala | Cys | Glu | Ser | Pro | Leu | Ala | Ala |
| | | | | 415 | | | | | 420 | | | | | 425 |
| Trp | Ser | Leu | Gly | Ile | Thr | Pro | Ala | Leu | Val | Leu | Gln | Met | Leu | Leu |
| | | | | 430 | | | | | 435 | | | | | 440 |
| Gly | Phe | Ile | Gly | Ala | Gly | Pro | Ser | Arg | Ala | Gly | Pro | Leu | Thr | Leu |
| | | | | 445 | | | | | 450 | | | | | 455 |

5 Pro Ala Trp Leu His Ser Pro *** Arg Leu Pro Leu Val His Pro
 460 465 470
 Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro
 475 480 485
 10 Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser *** Asp Val Gln Gly
 490 495 500
 Pro Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly Pro Trp Lys
 505 510 515
 Ser Pro Pro Pro His His *** Ser Ala Leu Thr Leu Gly Phe His
 520 525 530
 Gly Pro His Ser Thr Ala Ser Pro Thr *** Ala Cys Asp Leu Gly
 535 540 545
 Thr Lys Gly Gly Val Pro Arg Leu Leu *** Leu Ser Arg Gly Ser
 550 555 560
 15 Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly Gly Ser Ala His
 565 570 575
 Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys Ile Leu Glu
 580 585 590
 20 Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly Gln Cys
 595 600 605
 Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro Xxx
 610 615 620

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

40 Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
 1 5 10 15
 Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
 20 25 30
 Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
 35 40 45
 45 Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
 50 55 60
 Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
 65 70 75
 50 Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro
 80 85 90
 Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
 95 100 105
 Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
 110 115 120
 55 Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
 125 130 135
 Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
 140 145 150
 60 Cys Ala Val Leu Leu Ser Ala Val Gln Gln Ala Gln Ala Gly Trp
 155 160 165
 Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys
 170 175 180
 Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly
 185 190 195
 65 Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala
 200 205 210

| | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Lys | Pro | Asn | Ile | Phe | His | Lys | Asp | Pro | Asp | Val | Asn | Met | Leu | His |
| | | | | | 215 | | | | | 220 | | | | | 225 |
| | Val | Phe | Val | Leu | Gly | Glu | Trp | Gln | Pro | Ile | Glu | Tyr | Gly | Lys | Lys |
| | | | | | 230 | | | | | 235 | | | | | 240 |
| 5 | Lys | Leu | Lys | Tyr | Leu | Pro | Tyr | Asn | His | Gln | His | Glu | Tyr | Phe | Phe |
| | | | | | 245 | | | | | 250 | | | | | 255 |
| | Leu | Ile | Gly | Pro | Pro | Leu | Leu | Ile | Pro | Met | Tyr | Phe | Gln | Tyr | Gln |
| | | | | | 260 | | | | | 265 | | | | | 270 |
| 10 | Ile | Ile | Met | Thr | Met | Ile | Val | His | Lys | Asn | Trp | Val | Asp | Leu | Ala |
| | | | | | 275 | | | | | 280 | | | | | 285 |
| | Trp | Ala | Val | Ser | Tyr | Tyr | Ile | Arg | Phe | Phe | Ile | Thr | Tyr | Ile | Pro |
| | | | | | 290 | | | | | 295 | | | | | 300 |
| | Phe | Tyr | Gly | Ile | Leu | Gly | Ala | Leu | Leu | Phe | Leu | Asn | Phe | Ile | Arg |
| | | | | | 305 | | | | | 310 | | | | | 315 |
| 15 | Phe | Leu | Glu | Ser | His | Trp | Phe | Val | Trp | Val | Thr | Gln | Met | Asn | His |
| | | | | | 320 | | | | | 325 | | | | | 330 |
| | Ile | Val | Met | Glu | Ile | Asp | Gln | Glu | Ala | Tyr | Arg | Asp | Trp | Phe | Ser |
| | | | | | 335 | | | | | 340 | | | | | 345 |
| 20 | Ser | Gln | Leu | Thr | Ala | Thr | Cys | Asn | Val | Glu | Gln | Ser | Phe | Phe | Asn |
| | | | | | 350 | | | | | 355 | | | | | 360 |
| | Asp | Trp | Phe | Ser | Gly | His | Leu | Asn | Phe | Gln | Ile | Glu | His | His | Leu |
| | | | | | 365 | | | | | 370 | | | | | 375 |
| | Phe | Pro | Thr | Met | Pro | Arg | His | Asn | Leu | His | Lys | Ile | Ala | Pro | Leu |
| | | | | | 380 | | | | | 385 | | | | | 390 |
| 25 | Val | Lys | Ser | Leu | Cys | Ala | Lys | His | Gly | Ile | Glu | Tyr | Gln | Glu | Lys |
| | | | | | 400 | | | | | 405 | | | | | 410 |
| | Pro | Leu | Leu | Arg | Ala | Leu | Leu | Asp | Ile | Ile | Arg | Ser | Leu | Lys | Lys |
| | | | | | 415 | | | | | 420 | | | | | 425 |
| 30 | Ser | Gly | Lys | Leu | Trp | Leu | Asp | Ala | Tyr | Leu | His | Lys | *** | Ser | His |
| | | | | | 430 | | | | | 435 | | | | | 440 |
| | Ser | Pro | Arg | Asp | Thr | Val | Gly | Lys | Gly | Cys | Arg | Trp | Gly | Asp | Gly |
| | | | | | 445 | | | | | 450 | | | | | 455 |
| | Gln | Arg | Asn | Asp | Gly | Leu | Leu | Phe | *** | Gly | Val | Ser | Glu | Arg | Leu |
| | | | | | 460 | | | | | 465 | | | | | 470 |
| 35 | Val | Tyr | Ala | Leu | Leu | Thr | Asp | Pro | Met | Leu | Asp | Leu | Ser | Pro | Phe |
| | | | | | 475 | | | | | 480 | | | | | 485 |
| | Leu | Leu | Ser | Phe | Phe | Ser | Ser | His | Leu | Pro | His | Ser | Thr | Leu | Pro |
| | | | | | 490 | | | | | 495 | | | | | 500 |
| 40 | Ser | Trp | Asp | Leu | Pro | Ser | Leu | Ser | Arg | Gln | Pro | Ser | Ala | Met | Ala |
| | | | | | 505 | | | | | 510 | | | | | 515 |
| | Leu | Pro | Val | Pro | Pro | Ser | Pro | Phe | Phe | Gln | Gly | Ala | Glu | Arg | Trp |
| | | | | | 520 | | | | | 525 | | | | | 530 |
| | Pro | Pro | Gly | Val | Ala | Leu | Ser | Tyr | Leu | His | Ser | Leu | Pro | Leu | Lys |
| | | | | | 535 | | | | | 540 | | | | | 545 |
| 45 | Met | Gly | Gly | Asp | Gln | Arg | Ser | Met | Gly | Leu | Ala | Cys | Glu | Ser | Pro |
| | | | | | 550 | | | | | 555 | | | | | 560 |
| | Leu | Ala | Ala | Trp | Ser | Leu | Gly | Ile | Thr | Pro | Ala | Leu | Val | Leu | Gln |
| | | | | | 565 | | | | | 570 | | | | | 575 |
| 50 | Met | Leu | Leu | Gly | Phe | Ile | Gly | Ala | Gly | Pro | Ser | Arg | Ala | Gly | Pro |
| | | | | | 580 | | | | | 585 | | | | | 590 |
| | Leu | Thr | Leu | Pro | Ala | Trp | Leu | His | Ser | Pro | *** | Arg | Leu | Pro | Leu |
| | | | | | 595 | | | | | 600 | | | | | 605 |
| | Val | His | Pro | Phe | Ile | Glu | Arg | Pro | Ala | Leu | Leu | Gln | Ser | Ser | Gly |
| | | | | | 610 | | | | | 615 | | | | | 620 |
| 55 | Leu | Pro | Pro | Ala | Ala | Arg | Leu | Ser | Thr | Arg | Gly | Leu | Ser | *** | Asp |
| | | | | | 625 | | | | | 630 | | | | | 635 |
| | Val | Gln | Gly | Pro | Arg | Pro | Ala | Gly | Thr | Ala | Ser | Pro | Asn | Leu | Gly |
| | | | | | 640 | | | | | 645 | | | | | 650 |
| 60 | Pro | Trp | Lys | Ser | Pro | Pro | Pro | His | His | *** | Ser | Ala | Leu | Thr | Leu |
| | | | | | 655 | | | | | 660 | | | | | 665 |
| | Gly | Phe | His | Gly | Pro | His | Ser | Thr | Ala | Ser | Pro | Thr | *** | Ala | Cys |
| | | | | | 670 | | | | | 675 | | | | | 680 |
| | Asp | Leu | Gly | Thr | Lys | Gly | Gly | Val | Pro | Arg | Leu | Leu | *** | Leu | Ser |
| | | | | | 685 | | | | | 690 | | | | | 695 |
| 65 | Arg | Gly | Ser | Gly | His | Val | Gln | Gly | Gly | Ala | Gly | Trp | Pro | Gly | Gly |
| | | | | | 700 | | | | | 705 | | | | | 710 |

5 Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys
715 720 725
Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala
730 735 740
Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val
745 750 755
Gly Pro Xxx

SEQUENCE LISTING

- 5 (1) GENERAL INFORMATION:
- 10 (i) APPLICANT: KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
LEONARD, AMANDA
- 15 (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
- (iii) NUMBER OF SEQUENCES: 40
- 20 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LIMBACH AND LIMBACH LLP
(B) STREET: 2001 FERRY BUILDING
(C) CITY: SAN FRANCISCO
(D) STATE: CA
(E) COUNTRY: USA
25 (F) ZIP: 94111
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
30 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
35 (B) (B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: WARD, MICHAEL R.
(B) REGISTRATION NUMBER: 38,651
(C) REFERENCE/DOCKET NUMBER: CGAB-210
- (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: (415) 433-4150
(B) TELEFAX: (415) 433-8716
(C) TELEX: N/A
- 50 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 CGACACTCCT TCCTTCTTCT CACCCGTCCT AGTCCCCTTC AACCCCCCTC TTTGACAAAG 60
 ACAACAAACC ATGGCTGCTG CTCCCAGTGT GAGGACGTTT ACTCGGGCCG AGGTTTTGAA 120
 TGCCGAGGCT CTGAATGAGG GCAAGAAGGA TGCCGAGGCA CCCTTCTTGA TGATCATCGA 180
 CAACAAGGTG TACGATGTCC GCGAGTTCGT CCCTGATCAT CCCGGTGGAA GTGTGATTCT 240
 10 CACGCACGTT GGCAAGGACG GCACTGACGT CTTTGACACT TTTACCCCCG AGGCTGCTTG 300
 GGAGACTCTT GCCAACTTTT ACGTTGGTGA TATTGACGAG AGCGACCGCG ATATCAAGAA 360
 TGATGACTTT GCGGCCGAGG TCCGCAAGCT GCGTACCTTG TTCCAGTCTC TTGGTTACTA 420
 15 CGATTCTTCC AAGGCATACT ACGCCTTCAA GGTCTCGTTC AACCTCTGCA TCTGGGGTTT 480
 GTCGACGGTC ATTGTGGCCA AGTGGGGCCA GACCTCGACC CTCGCCAACG TGCTCTCGGC 540
 TGCGCTTTTG GGTCTGTTCT GGCAGCAGTG CGGATGGTTG GCTCACGACT TTTTGCATCA 600
 20 CCAGGTCTTC CAGGACCGTT TCTGGGGTGA TCTTTTCGGC GCCTTCTTGG GAGGTGTCTG 660
 CCAGGGCTTC TCGTCCTCGT GGTGGAAGGA CAAGCACAAAC ACTCACCACG CCGCCCCCAA 720
 25 CGTCCACGGC GAGGATCCCG ACATTGACAC CCACCCTCTG TTGACCTGGA GTGAGCATGC 780
 GTTGAGAGTG TTCTCGGATG TCCCAGATGA GGAGCTGACC CGCATGTGGT CGCGTTTCAT 840
 GGTCTGAAC CAGACCTGGT TTTACTTCCC CATCTCTCTG TTTGCCCGTC TCTCCTGGTG 900
 30 CCTCCAGTCC ATTCTCTTTC TGCTGCCTAA CGGTCAGGCC CACAAGCCCT CGGGCGCGCG 960
 TGTGCCCATC TCGTTGGTCG AGCAGCTGTC GCTTGCGATG CACTGGACCT GGTACCTCGC 1020
 35 CACCATGTTC CTGTTTCATCA AGGATCCCGT CAACATGCTG GTGTACTTTT TGGTGTGCGA 1080
 GGCGGTGTGC GGAAACTTGT TGGCGATCGT GTTCTCGCTC AACCAACAACG GTATGCCTGT 1140
 GATCTCGAAG GAGGAGGCGG TCGATATGGA TTTCTTCACG AAGCAGATCA TCACGGGTCG 1200
 40 TGATGTCCAC CCGGTCTAT TTGCCAACTG GTTCACGGGT GGATTGAACT ATCAGATCGA 1260
 GCACCACTTG TTCCCTTCGA TGCTCGCCA CAACTTTTCA AAGATCCAGC CTGCTGTCGA 1320
 45 GACCCTGTGC AAAAAGTACA ATGTCCGATA CCACACCACC GGTATGATCG AGGGAAGTGC 1380
 AGAGGTCTTT AGCCGTCTGA ACGAGGTCTC CAAGGCTGCC TCCAAGATGG GTAAGGCGCA 1440
 GTAAAAA AAAACAAGGAC GTTTTTTTTC GCCAGTGCCT GTGCCTGTGC CTGCTTCCCT 1500
 50 TGTCAAGTCG AGCGTTTCTG GAAAGGATCG TTCAGTGCAG TATCATCATT CTCCTTTTAC 1560
 CCCCCGCTCA TATCTCATTC ATTTCTCTTA TTAAACAAC TGTTCCCCCC TTCACCG 1617

55 (2) INFORMATION FOR SEQ ID NO:2:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 457 amino acids
 (B) TYPE: amino acid
 60 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu
1 . 5 10 15

Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
20 25 30

10 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
35 40 45

15 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
50 55 60

Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
65 70 75 80

20 Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
85 90 95

Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
100 105 110

25 Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
115 120 125

30 Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
130 135 140

Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
145 150 155 160

35 Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
165 170 175

His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
180 185 190

40 Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
195 200 205

His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
210 215 220

Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
225 230 235 240

50 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
245 250 255

Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
260 265 270

55 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
275 280 285

Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
290 295 300

Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
305 310 315 320

65 Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser

-145-

SUBSTITUTE SHEET

| | 325 | 330 | 335 |
|----|---|---------------------------------|-----|
| 5 | Gln Ala Val Cys Gly Asn Leu Leu | Ala Ile Val Phe Ser Leu Asn His | |
| | 340 | 345 | 350 |
| | Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe | | |
| | 355 | 360 | 365 |
| 10 | Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe | | |
| | 370 | 375 | 380 |
| | Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu | | |
| | 385 | 390 | 395 |
| 15 | Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val | | |
| | 405 | 410 | 415 |
| | Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met | | |
| | 420 | 425 | 430 |
| 20 | Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys | | |
| | 435 | 440 | 445 |
| | Ala Ala Ser Lys Met Gly Lys Ala Gln | | |
| 25 | 450 | 455 | |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCCCTGTC | GCTGTCGGCA | CACCCCATCC | TCCCTCGCTC | CCTCTGCGTT | TGTCCTTGGC | 60 |
| CCACCGTCTC | TCCTCCACCC | TCCGAGACGA | CTGCAACTGT | AATCAGGAAC | CGACAAATAC | 120 |
| ACGATTTCTT | TTTACTCAGC | ACCAACTCAA | AATCCTCAAC | CGCAACCCTT | TTTCAGGATG | 180 |
| GCACCTCCCA | ACACTATCGA | TGCCGGTTTG | ACCCAGCGTC | ATATCAGCAC | CTCGGCCCCA | 240 |
| AACTCGGCCA | AGCCTGCCTT | CGAGCGCAAC | TACCAGCTCC | CCGAGTTCAC | CATCAAGGAG | 300 |
| ATCCGAGAGT | GCATCCCTGC | CCACTGCTTT | GAGCGCTCCG | GTCTCCGTGG | TCTCTGCCAC | 360 |
| GTTGCCATCG | ATCTGACTTG | GGCGTCGCTC | TTGTTCTTGG | CTGCGACCCA | GATCGACAAG | 420 |
| TTTGAGAATC | CCTTGATCCG | CTATTTGGCC | TGGCCTGTTT | ACTGGATCAT | GCAGGGTATT | 480 |
| GTCTGCACCG | GTGTCTGGGT | GCTGGCTCAC | GAGTGTGGTC | ATCAGTCCTT | CTCGACCTCC | 540 |
| AAGACCCTCA | ACAACACAGT | TGGTTGGATC | TTGCACTCGA | TGCTCTTGGT | CCCCTACCAC | 600 |
| TCCTGGAGAA | TCTCGCACTC | GAAGCACCAC | AAGGCCACTG | GCCATATGAC | CAAGGACCAG | 660 |
| GTCTTTGTGC | CCAAGACCCG | CTCCCAGGTT | GGCTTGCCTC | CCAAGGAGAA | CGCTGCTGCT | 720 |

GCCGTTCAGG AGGAGGACAT GTCCGTGCAC CTGGATGAGG AGGCTCCCAT TGTGACTTTG 780
 TTCTGGATGG TGATCCAGTT CTTGTTTCGGA TGGCCCGCGT ACCTGATTAT GAACGCCTCT 840
 5 GGCCAAGACT ACGGCCGCTG GACCTCGCAC TTCCACACGT ACTCGCCCAT CTTTGAGCCC 900
 CGCAACTTTT TCGACATTAT TATCTCGGAC CTCGGTGTGT TGGCTGCCCT CGGTGCCCTG 960
 10 ATCTATGCCT CCATGCAGTT GTCGCTCTTG ACCGTCACCA AGTACTATAT TGTCCCCTAC 1020
 CTCTTTGTCA ACTTTTGGTT GGTCTGATC ACCTTCTTGC AGCACACCGA TCCCAAGCTG 1080
 CCCCATTACC GCGAGGGTGC CTGGAATTC CAGCGTGGAG CTCTTTGCAC CGTTGACCGC 1140
 15 TCGTTTGGCA AGTTCTTGA CCATATGTT CACGGCATTG TCCACACCCA TGTGGCCCAT 1200
 CACTTGTTCT CGCAAATGCC GTTCTACCAT GCTGAGGAAG CTACCTATCA TCTCAAGAAA 1260
 20 CTGCTGGGAG AGTACTATGT GTACGACCCA TCCCCGATCG TCGTTGCGGT CTGGAGGTCG 1320
 TTCCGTGAGT GCCGATTCGT GGAGGATCAG GGAGACGTGG TCTTTTCAA GAAGTAAAAA 1380
 AAAAGACAAT GGACCACACA CAACCTTGTC TCTACAGACC TACGTATCAT GTAGCCATAC 1440
 25 CACTTCATAA AAGAACATGA GCTCTAGAGG CGTGTCATTC GCGCCTCC 1488

(2) INFORMATION FOR SEQ ID NO:4:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile
 1 5 10 15
 45 Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr
 20 25 30
 Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
 35 40 45
 50 His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
 50 55 60
 Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp
 65 70 75 80
 Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
 85 90 95
 60 Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
 100 105 110
 Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val
 115 120 125
 65

| | | |
|----|---|-----------------|
| | Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg | |
| | 130 | 135 140 |
| 5 | Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp | |
| | 145 | 150 155 160 |
| | Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys | |
| | | 165 170 175 |
| 10 | Glu Asn Ala Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu | |
| | | 180 185 190 |
| | Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe | |
| | | 195 200 205 |
| 15 | Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp | |
| | | 210 215 220 |
| | Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu | |
| | | 225 230 235 240 |
| | Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala | |
| | | 245 250 255 |
| 25 | Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr | |
| | | 260 265 270 |
| | Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu | |
| | | 275 280 285 |
| 30 | Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr | |
| | | 290 295 300 |
| | Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp | |
| | | 305 310 315 320 |
| 35 | Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His | |
| | | 325 330 335 |
| 40 | Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala | |
| | | 340 345 350 |
| | Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val | |
| | | 355 360 365 |
| 45 | Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu | |
| | | 370 375 380 |
| 50 | Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys | |
| | | 385 390 395 |

(2) INFORMATION FOR SEQ ID NO:5:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: peptide

- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Glu | Val | Arg | Lys | Leu | Arg | Thr | Leu | Phe | Gln | Ser | Leu | Gly | Tyr | Tyr | Asp | |
| | 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| 5 | Ser | Ser | Lys | Ala | Tyr | Tyr | Ala | Phe | Lys | Val | Ser | Phe | Asn | Leu | Cys | Ile | |
| | | | | 20 | | | | | 25 | | | | | 30 | | | |
| | Trp | Gly | Leu | Ser | Thr | Val | Ile | Val | Ala | Lys | Trp | Gly | Gln | Thr | Ser | Thr | |
| | | | 35 | | | | | 40 | | | | | 45 | | | | |
| 10 | Leu | Ala | Asn | Val | Leu | Ser | Ala | Ala | Leu | Leu | Gly | Leu | Phe | Trp | Gln | Gln | |
| | | 50 | | | | | 55 | | | | | 60 | | | | | |
| | Cys | Gly | Trp | Leu | Ala | His | Asp | Phe | Leu | His | His | Gln | Val | Phe | Gln | Asp | |
| 15 | 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| | Arg | Phe | Trp | Gly | Asp | Leu | Phe | Gly | Ala | Phe | Leu | Gly | Gly | Val | Cys | Gln | |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| 20 | Gly | Phe | Ser | Ser | Ser | Trp | Trp | Lys | Asp | Lys | His | Asn | Thr | His | His | Ala | |
| | | | | 100 | | | | | 105 | | | | | 110 | | | |
| | Ala | Pro | Asn | Val | His | Gly | Glu | Asp | Pro | Asp | Ile | Asp | Thr | His | Pro | Leu | |
| 25 | | | | 115 | | | | 120 | | | | | 125 | | | | |
| | Leu | Thr | Trp | Ser | Glu | His | Ala | Leu | Glu | Met | Phe | Ser | Asp | Val | Pro | Asp | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| | Glu | Glu | Leu | Thr | Arg | Met | Trp | Ser | Arg | Phe | Met | Val | Leu | Asn | Gln | Thr | |
| 30 | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| | Trp | Phe | Tyr | Phe | Pro | Ile | Leu | Ser | Phe | Ala | Arg | Leu | Ser | Trp | Cys | Leu | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| 35 | Gln | Ser | Ile | Leu | Phe | Val | Leu | Pro | Asn | Gly | Gln | Ala | His | Lys | Pro | Ser | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| | Gly | Ala | Arg | Val | Pro | Ile | Ser | Leu | Val | Glu | Gln | Leu | Ser | Leu | Ala | Met | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 40 | His | Trp | Thr | Trp | Tyr | Leu | Ala | Thr | Met | Phe | Leu | Phe | Ile | Lys | Asp | Pro | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| | Val | Asn | Met | Leu | Val | Tyr | Phe | Leu | Val | Ser | Gln | Ala | Val | Cys | Gly | Asn | |
| 45 | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| | Leu | Leu | Ala | Ile | Val | Phe | Ser | Leu | Asn | His | Asn | Gly | Met | Pro | Val | Ile | |
| | | | | 245 | | | | | | 250 | | | | | 255 | | |
| 50 | Ser | Lys | Glu | Glu | Ala | Val | Asp | Met | Asp | Phe | Phe | Thr | Lys | Gln | Ile | Ile | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| | Thr | Gly | Arg | Asp | Val | His | Pro | Gly | Leu | Phe | Ala | Asn | Trp | Phe | Thr | Gly | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| 55 | Gly | Leu | Asn | Tyr | Gln | Ile | Glu | His | His | Leu | Phe | Pro | Ser | Met | Pro | Arg | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| | His | Asn | Phe | Ser | Lys | Ile | Gln | Pro | Ala | Val | Glu | Thr | Leu | Cys | Lys | Lys | |
| 60 | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| | Tyr | Asn | Val | Arg | Tyr | His | Thr | Thr | Gly | Met | Ile | Glu | Gly | Thr | Ala | Glu | |
| | | | | | 325 | | | | | 330 | | | | | 335 | | |
| 65 | Val | Phe | Ser | Arg | Leu | Asn | Glu | Val | Ser | Lys | Ala | Ala | Ser | Lys | Met | Gly | |

340

345

350

Lys Ala Gln
355

5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Thr Leu Tyr Thr Leu Ala Phe Val Ala Ala Asn Ser Leu Gly Val
1 5 10 15

25

Leu Tyr Gly Val Leu Ala Cys Pro Ser Val Xaa Pro His Gln Ile Ala
20 25 30

30

Ala Gly Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile Gly Xaa
35 40 45

35

Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Asn Asn Xaa Phe
50 55 60

Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ile Ala Trp Trp
65 70 75 80

Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp Tyr
85 90 95

40

Gly Pro Asn Leu Gln His Ile Pro
100

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Val Leu Tyr Gly Val Leu Ala Cys Thr Ser Val Phe Ala His Gln
1 5 10 15

60

Ile Ala Ala Ala Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile
20 25 30

65

Gly His Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Tyr Asn
35 40 45

Trp Phe Glu Lys Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser
 65 70 75 80
 5 Tyr Met Asp Trp Phe Phe Cys Gly Leu Gln Phe Gln Leu Glu His His
 85 90 95
 Leu Phe Pro Arg Leu Pro Arg Cys His Leu Arg Lys Val Ser Pro Val
 100 105 110
 10 Gly Gln Arg Gly Phe Gln Arg Lys Xaa Asn Leu Ser Xaa
 115 120 125

(2) INFORMATION FOR SEQ ID NO:9:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30 Pro Ala Thr Glu Val Gly Gly Leu Ala Trp Met Ile Thr Phe Tyr Val
 1 5 10 15
 Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
 20 25 30
 35 Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn Trp Phe Val Trp
 35 40 45
 Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
 50 55 60
 40 Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
 65 70 75 80
 45 Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
 85 90 95
 His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala
 100 105 110
 50 Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
 115 120 125
 Lys Pro Leu
 130

(2) INFORMATION FOR SEQ ID NO:10:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ser | Pro | Lys | Ser | Ser | Pro | Thr | Arg | Asn | Met | Thr | Pro | Ser | Pro | Phe |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ile | Asp | Trp | Leu | Trp | Gly | Gly | Leu | Asn | Tyr | Gln | Ile | Glu | His | His | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Pro | Thr | Met | Pro | Arg | Cys | Asn | Leu | Asn | Arg | Cys | Met | Lys | Tyr | Val |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Lys | Glu | Trp | Cys | Ala | Glu | Asn | Asn | Leu | Pro | Tyr | Leu | Val | Asp | Asp | Tyr |
| | | | 50 | | | 55 | | | | | 60 | | | | |
| Phe | Val | Gly | Tyr | Asn | Leu | Asn | Leu | Gln | Gln | Leu | Lys | Asn | Met | Ala | Glu |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 |
| Leu | Val | Gln | Ala | Lys | Ala | Ala | | | | | | | | | |
| | | | | | | 85 | | | | | | | | | |

25 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | His | Glu | Ala | Ala | Arg | Gly | Gly | Thr | Arg | Leu | Ala | Tyr | Met | Leu | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Cys | Met | Gln | Trp | Thr | Asp | Leu | Leu | Trp | Ala | Ala | Ser | Phe | Tyr | Ser | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Phe | Leu | Ser | Tyr | Ser | Pro | Phe | Tyr | Gly | Ala | Thr | Gly | Thr | Leu | Leu |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Leu | Phe | Val | Ala | Val | Arg | Val | Leu | Glu | Ser | His | Trp | Phe | Val | Trp | Ile |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Thr | Gln | Met | Asn | His | Ile | Pro | Lys | Glu | Ile | Gly | His | Glu | Lys | His | Arg |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 |
| Asp | Trp | Ala | Ser | Ser | Gln | Leu | Ala | Ala | Thr | Cys | Asn | Val | Glu | Pro | Ser |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Phe | Ile | Asp | Trp | Phe | Ser | Gly | His | Leu | Asn | Phe | Gln | Ile | Glu | His |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| His | Leu | Phe | Pro | Thr | Met | Thr | Arg | His | Asn | Tyr | Arg | Xaa | Val | Ala | Pro |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Val | Lys | Ala | Phe | Cys | Ala | Lys | His | Gly | Leu | His | Tyr | Glu | Val | |
| | | 130 | | | | 135 | | | | | 140 | | | | |

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCAAGCTTCT GCAGGAGCTC TTTTTTTTTT TTTT

35

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CUACUACUAC UAGGAGTCCT CTACGGTGTT TTG

33

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAUCAUCAUC AUATGATGCT CAAGCTGAAA CTG

33

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

-154-

SUBSTITUTE SHEET

TACCAACTCG AGAAAATGGC TGCTGCTCCC AGTGTGAGG

39

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACTGATCTA GATTACTGCG CCTTACCCAT CTTGGAGGC

39

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TACCAACTCG AGAAAATGGC ACCTCCCAAC ACTATCGAT

39

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AACTGATCTA GATTACTTCT TGAAAAAGAC CACGTCTCC

39

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 746 nucleic acids
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 CGTATGTCAC TCCATTCCAA ACTCGTTCAT GGTATCATAA ATATCAACAC ATTTACGCTC 60
CACTCCTCTA TGGTATTTAC AACTCAAAT ATCGTACTCA AGATTGGGAA GCTTTTGTA 120
AGGATGGTAA AAATGGTGCA ATTCGTGTTA GTGTCGCCAC AAATTTTCGAT AAGGCCGCTT 180
ACGTCATTGG TAAATTGTCT TTTGTTTTCT TCCGTTTCAT CCTTCCACTC CGTTATCATA 240
GCTTTACAGA TTTAATTTGT TATTCCTCA TTGCTGAATT CGTCTTTGGT TGGTATCTCA 300
CAATTAATTT CCAAGTTAGT CATGTCGCTG AAGATCTCAA ATTCTTTGCT ACCCCTGAAA 360
10 GACCAGATGA ACCATCTCAA ATCAATGAAG ATTGGGCAAT CCTTCAACTT AAAACTACTC 420
AAGATTATGG TCATGGTTCA CTCCTTTGTA CCTTTTTCAG TGGTTCTTTA AATCATCAAG 480
TTGTTTCATCA TTTATTCCCA TCAATTGCTC AAGATTTCCTA CCCACAACTT GTACCAATTG 540
TAAAAGAAGT TTGTAAAGAA CATAACATTA CTTACCACAT TAAACCAAAC TTCACTGAAG 600
CTATTATGTC ACACATTAAT TACCTTTACA AAATGGGTAA TGATCCAGAT TATGTTAAAA 660
15 AACCATTAGC CTCAAAGAT GATTAAATGA AATAACTTAA AAACCAATTA TTTACTTTTG 720
ACAAACAGTA ATATTAATAA ATACAA 746

(2) INFORMATION FOR SEQ ID NO:20:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30 Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln
1 5 10 15
His Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr
20 25 30
35 Arg Thr Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly
35 40 45
Ala Ile Arg Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr
50 55 60
Val Ile Gly Lys Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro
65 70 75
40 Leu Arg Tyr His Ser Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile
80 85 90
Ala Glu Phe Val Phe Gly Trp Tyr Leu Thr Ile Asn Phe Gln Val
95 100 105
45 Ser His Val Ala Glu Asp Leu Lys Phe Phe Ala Thr Pro Glu Arg
110 115 120
Pro Asp Glu Pro Ser Gln Ile Asn Glu Asp Trp Ala Ile Leu Gln
125 130 135
Leu Lys Thr Thr Gln Asp Tyr Gly His Gly Ser Leu Leu Cys Thr
140 145 150
50 Phe Phe Ser Gly Ser Leu Asn His Gln Val Val His His Leu Phe
155 160 165
Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu Val Pro Ile Val
170 175 180
55 Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His Ile Lys Pro
185 190 195
Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu Tyr Lys
200 205 210
Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser Lys
215 220 225
60 Asp Asp Xaa

(2) INFORMATION FOR SEQ ID NO 21:

65 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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| | | | | | | |
|-------------|-------------|-------------|------------|------------|------------|-----|
| TTTTGGAAGG | NTCCAAGTTN | ACCACGGANT | NGGCAAGTTN | ACGGGGCGGA | AANCGGTTTT | 60 |
| CCCCCAAGC | CTTTTGTGCA | CTGGTCTGT | GGTGGCTTCC | AGTACCAAGT | CGACCACCAC | 120 |
| TTATCCCCA | GCCTGCCCGG | ACACAATCTG | GCCAAGACAC | ACGCACTGGT | CGAATCGTTC | 180 |
| TGCAAGGAGT | GGGGTGTCCA | GTACCACGAA | GCCGACCTCG | TGGACGGGAC | CATGGAAGTC | 240 |
| TTGCACCATT | TGGGCAGCGT | GGCCGGCGAA | TTCGTCGTGG | ATTTTGTACG | CGACGGACCC | 300 |
| GCCATGTAAT | CGTCGTTCGT | GACGATGCAA | GGGTTACGCG | ACATCTACAC | ACACTCACTC | 360 |
| ACACAAC TAG | TGTAAC TCGT | ATAGAATT CG | GTGTCGACCT | GGACCTGTGT | TGACTGGTTG | 420 |
| GGGATAGGGT | AGGTAGGCGG | ACGCGTGGGT | CGNCCCCGGG | AATTCTGTGA | CCGGTACCTG | 480 |
| CCCCGCGTNA | AAGT | | | | | 494 |

(2) INFORMATION FOR SEQ ID NO:22:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Phe | Trp | Lys | Xaa | Pro | Ser | Xaa | Pro | Arg | Xaa | Xaa | Gln | Val | Xaa | Gly | 1 | 5 | 10 | 15 |
| Ala | Glu | Xaa | Gly | Phe | Pro | Pro | Lys | Pro | Phe | Val | Asp | Trp | Phe | Cys | 20 | 25 | 30 | 35 |
| Gly | Gly | Phe | Gln | Tyr | Gln | Val | Asp | His | His | Leu | Phe | Pro | Ser | Leu | 40 | 45 | 50 | 55 |
| Pro | Arg | His | Asn | Leu | Ala | Lys | Thr | His | Ala | Leu | Val | Glu | Ser | Phe | 60 | 65 | 70 | 75 |
| Cys | Lys | Glu | Trp | Gly | Val | Gln | Tyr | His | Glu | Ala | Asp | Leu | Val | Asp | 80 | 85 | | |
| Gly | Thr | Met | Glu | Val | Leu | His | His | Leu | Gly | Ser | Val | Ala | Gly | Glu | | | | |
| Phe | Val | Val | Asp | Phe | Val | Arg | Asp | Gly | Pro | Ala | Met | | | | | | | |

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 nucleic acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: nucleic acid

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

5 GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCGACGTG GTTTAAGCGT CATGGGTGCG 60
 CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTACTTGT GCGCCTTTGG TCTCGGCTGC 120
 ATTTACATT TTCTGCAGTT CGCCGTAAGT CACACCCATT TGCCCGTGAG CAACCCGGAG 180
 GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCACACTGT GAACATCAGC ACCAAGTCGT 240
 GGTTCGTAC ATGGTGGATG TCGAACCTCA ACTTTCAGAT CGAGCACCAC CTTTTCCCA 300
 CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCGCGCGT CGAGGCCCTC TTCAAGCGCC 360
 10 ACGGTCTCCC TTACTACGAC ATGCCCTACA CGAGCGCCGT CTCCACCACC TTTGCCAACC 420
 TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAGCGCGA CTAGCCTCTT TTCCTAGACC 480
 TTAATTCCTCC ACCCCACCCC ATGTTCTGTC TTCCTCCCGC 520

15 (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys
 1 5 10 15
 30 Arg His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His
 20 25 30
 Val Leu Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala
 35 40 45
 Val Arg Arg Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly
 50 55 60
 35 Ser Ala Ala Leu Ala Arg Val Arg Ala Asp His Thr Val Asn Ile
 65 70 75
 Ser Thr Lys Ser Trp Phe Val Thr Trp Trp Met Ser Asn Leu Asn
 80 85 90
 40 Phe Gln Ile Glu His His Leu Phe Pro Thr Ala Pro Gln Phe Arg
 95 100 105
 Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu Phe Lys Arg His
 110 115 120
 Gly Leu Pro Tyr Tyr Asp Met Pro Tyr Thr Ser Ala Val Ser Thr
 125 130 135
 45 Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly Asp Ala
 140 145 150
 Lys Arg Asp

50 (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 nucleic acids
 55 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

65 ACGCGTCCGC CCACGCGTCC GCCGCGAGCA ACTCATCAAG GAAGGCTACT TTGACCCCTC 60
 GCTCCCGCAC ATGACGTACC GCGTGGTCGA GATTGTTGTT CTCTTCGTGC TTTCTTTTG 120

5 GCTGATGGGT CAGTCTTCAC CCCTCGCGCT CGCTCTCGGC ATTGTCGTCA GCGGCATCTC 180
 TCAGGGTCGC TGCGGCTGGG TAATGCATGA GATGGGCCAT GGGTCGTTCA CTGGTGTCTAT 240
 TTGGCTTGAC GACCGGTTGT GCGAGTTCTT TTACGGCGTT GGTGTGGCA TGAGCGGTCA 300
 TTAAGTGGAAA AACCAGCACA GCAAACACCA CGCAGCGCCA AACCAGGCTCG AGCAGCATGT 360
 AGATCTCAAC ACCTTGCCAT TGGTGGCCTT CAACGAGCGC GTCGTGCGCA AGGTCCGACC 420

10 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly
 1 5 10 15
 Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu
 20 25 30
 Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser
 35 40 45
 Ser Pro Leu Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser
 50 55 60
 Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser
 65 70 75
 Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe
 80 85 90
 Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln
 95 100 105
 His Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val
 110 115 120
 Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val
 125
 Arg Lys Val Arg Pro

45 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2692004)

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCACGCCGAC CGGCGCCGGG AGATCCTGGC AAAGTATCCA GAGATAAAGT CCTTGATGAA 60
 ACCTGATCCC AATTTGATAT GGATTATAAT TATGATGGTT CTCACCCAGT TGGGTGCATT 120
 TTACATAGTA AAAGACTTGG ACTGGAAATG GGTCAATATT GGGGCCTATG CGTTTGGCAG 180
 TTGCATTAAC CACTCAATGA CTCTGGCTAT TCATGAGATT GCCACAATG CTGCCTTTGG 240
 CAACTGCAAA GCAATGTGGA ATCCTGCTGTT TGGAAATGTTT GCTAATCTTC CTATTGGGAT 300

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|------------|------------|------------|------------|------------|-------------|------|
| TCCATATTCA | ATTCCTTTA | AGAGGTATCA | CATGGATCAT | CATCGGTACC | TTGGAGCTGA | 360 |
| TGGCGTCGAT | GTAGATATTC | CTACCGATTT | TGAGGGCTGG | TTCTTCTGTA | CCGCTTTCAG | 420 |
| AAAGTTTATA | TGGGTATTC | TTCAGCCTCT | CTTTTATGCC | TTTCGACCTC | TGTTTCATCAA | 480 |
| CCCCAAACCA | ATTACGTATC | TGGAAGTTAT | CAATACCGTG | GCACAGGTCA | CTTTTGACAT | 540 |
| TTTAATTTAT | TACTTTTGG | GAATTAAATC | CTTAGTCTAC | ATGTTGGCAG | CATCTTTACT | 600 |
| TGGCCTGGGT | TTGCACCCAA | TTTCTGGACA | TTTTATAGCT | GAGCATTACA | TGTTCTTAAA | 660 |
| GGGTCATGAA | ACTTACTCAT | ATTATGGGCC | TCTGAATTTA | CTTACCTTCA | ATGTGGGTTA | 720 |
| TCATAATGAA | CATCATGATT | TCCCCAACAT | TCCTGGAAAA | AGTCTTCCAC | TGGTGAGGAA | 780 |
| AATAGCAGCT | GAATACTATG | ACAACCTCCC | TCACTACAAT | TCCTGGATAA | AAGTACTGTA | 840 |
| TGATTTTGTG | ATGGATGATA | CAATAAGTCC | CTACTCAAGA | ATGAAGAGGC | ACCAAAAAGG | 900 |
| AGAGATGGTG | CTGGAGTAAA | TATCATTAGT | GCCAAAGGGA | TTCTTCTCCA | AAACTTTAGA | 960 |
| TGATAAAATG | GAATTTTGC | ATTATTAAAC | TTGAGACCAG | TGATGCTCAG | AAGCTCCCCT | 1020 |
| GGCACAATTT | CAGAGTAAGA | GCTCGGTGAT | ACCAAGAAGT | GAATCTGGCT | TTTAAACAGT | 1080 |
| CAGCCTGACT | CTGTACTGCT | CAGTTTCACT | CACAGGAAAC | TTGTGACTTG | TGTATTATCG | 1140 |
| TCATTGAGGA | TGTTTCACTC | ATGTCTGTCA | TTTTATAAGC | ATATCATTTA | AAAAGCTTCT | 1200 |
| AAAAAGCTAT | TCGCCAGG | | | | | 1219 |

35 (2) INFORMATION FOR SEQ ID NO:28:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 655 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2153526)

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

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| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTACCTTCTA | CGTCCGCTTC | TTCCTCACTT | ATGTGCCACT | ATTGGGGCTG | AAAGCTTCCT | 60 |
| GGGCCTTTTC | TTCATAGTCA | GGTTCCTGGA | AAGCAACTGG | TTTGTGTGGG | TGACACAGAT | 120 |
| GAACCATATT | CCCATGCACA | TTGATCATGA | CCGGAACATG | GACTGGGTTT | CCACCCAGCT | 180 |
| CCAGGCCACA | TGCAATGTCC | ACAAGTCTGC | CTTCAATGAC | TGGTTCAGTG | GACACCTCAA | 240 |
| CTTCCAGATT | GAGCACCATC | TTTTTCCCAC | GATGCCTCGA | CACAATTACC | ACAAAGTGGC | 300 |
| TCCCCTGGTG | CAGTCCTTGT | GTGCCAAGCA | TGGCATAGAG | TACCAGTCCA | AGCCCCTGCT | 360 |
| GTCAGCCTTC | GCCGACATCA | TCCACTCACT | AAAGGAGTCA | GGGCAGCTCT | GGCTAGATGC | 420 |
| CTATCTTCAC | CAATAACAAC | AGCCACCCTG | CCCAGTCTGG | AAGAAGAGGA | GGAAGACTCT | 480 |
| GGAGCCAAGG | CAGAGGGGAG | CTTGAGGGAC | AATGCCACTA | TAGTTTAATA | CTCAGAGGGG | 540 |

GTTGGGTTTG GGGACATAAA GCCTCTGACT CAAACTCCTC CCTTTTATCT TCTAGCCACA 600
 GTTCTAAGAC CCAAAGTGGG GGGTGGACAC AGAAGTCCCT AGGAGGGAAG GAGCT 655

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(2) INFORMATION FOR SEQ ID NO:29:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3506132)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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GTCTTTTACT TTGGCAATGG CTGGATTCTT ACCCTCATCA CGGCCTTTGT CCTTGCTACC 60
 TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120
 CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180
 AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240
 CCCGATGTGA ACATGCTGCA CGTGTTTGTG CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300
 AAGA 304

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(2) INFORMATION FOR SEQ ID NO:30:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 918 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

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CAGGGACCTA CCCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG 60
 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 CTGTCTCCAG AGCAGCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGGTC 420
 TTTGGGACGT CCTTTTGGC CTTCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGGCC 480
 CAGGCTGGCT GGCTGCAGCA TGACTTTGGG CACCTGTCGG TCTTCAGCAC CTCAAAGTGG 540
 AACCATCTGC TACATCATTT TGTGATTGGC CACCTGAAGG GGGCCCCCGC CAGTTGGTGG 600
 AACCACATGC ACTTCCAGCA CCATGCCAAG CCCAACTGCT TCCGCAAAGA CCCAGACATC 660

65

AACATGCATC CCTTCTTCTT TGCCTTGGGG AAGATCCTCT CTGTGGAGCT TGGGAAACAG 720
 AAGAAAAAAT ATATGCCGTA CAACCACCAG CACARATACT TCTTCCTAAT TGGGCCCCCA 780
 5 GCCTTGCTGC CTCTCTACTT CCAGTGGTAT ATTTTCTATT TTGTTATCCA GCGAAAGAAG 840
 TGGGTGGACT TGGCCTGGAT CAGCAAACAG GAATACGATG AAGCCGGGCT TCCATTGTCC 900
 10 ACCGCAAATG CTTCTAAA 918

(2) INFORMATION FOR SEQ ID NO:31:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1686 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2511785)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

25 GCCACTTAAA GGGTGCCTCT GCCAACTGGT GGAATCATCG CCACTTCCAG CACCACGCCA 60
 AGCCTAACAT CTTCCACAAG GATCCCGATG TGAACATGCT GCACGTGTTT GTTCTGGGCG 120
 30 AATGGCAGCC CATCGAGTAC GGCAAGAAGA AGCTGAAATA CCTGCCCTAC AATCACCAGC 180
 ACGAATACTT CTTCTGATT GGGCCGCCGC TGCTCATCCC CATGTATTTT CAGTACCAGA 240
 TCATCATGAC CATGATCGTC CATAAGAACT GGGTGGACCT GGCCTGGGCC GTCAGCTACT 300
 35 ACATCCGGTT CTTTCATCACC TACATCCCTT TCTACGGCAT CCTGGGAGCC CTCCTTTTCC 360
 TCAACTTCAT CAGGTTTCCTG GAGAGCCACT GGTTTGTGTG GGTACACAG ATGAATCACA 420
 40 TCGTCATGGA GATTGACCAG GAGGCCTACC GTGACTGGTT CAGTAGCCAG CTGACAGCCA 480
 CCTGCAACGT GGAGCAGTCC TTCTTCAACG ACTGGTTCAG TGGACACCTT AACTTCCAGA 540
 TTGAGACCA CCTCTTCCCC ACCATGCCCC GGCACAACCT ACACAAGATC GCCCCGCTGG 600
 45 TGAAGTCTCT ATGTGCCAAG CATGGCATTG AATACCAGGA GAAGCCGCTA CTGAGGGCCC 660
 TGCTGGACAT CATCAGGTCC CTGAAGAAGT CTGGGAAGCT GTGGCTGGAC GCCTACCTTC 720
 50 ACAAATGAAG CCACAGCCCC CGGGACACCG TGGGGAAGGG GTGCAGGTGG GGTGATGGCC 780
 AGAGGAATGA TGGGCTTTTG TTCTGAGGGG TGTCAGAGAG GCTGGTGTAT GCACTGCTCA 840
 CGGACCCCAT GTTGGATCTT TCTCCCTTTT TCCTCTCCTT TTTCTCTTCA CATCTCCCCC 900
 55 ATAGCACCCCT GCCCTCATGG GACCTGCCCT CCCTCAGCCG TCAGCCATCA GCCATGGCCC 960
 TCCCAGTGCC TCCTAGCCCC TTCTTCCAAG GAGCAGAGAG GTGGCCACCG GGGGTGGCTC 1020
 60 TGTCCTACCT CCACTCTCTG CCCCTAAAGA TGGGAGGAGA CCAGCGGTCC ATGGGTCTGG 1080
 CCTGTGAGTC TCCCCTTGCA GCCTGGTCAC TAGGCATCAC CCCCCTTTG GTTCTTCAGA 1140
 TGCTCTTGGG GTTCATAGGG GCAGGTCCTA GTCGGGCAGG GCCCCTGACC CTCCCGGCCT 1200
 65 GGCTTCACTC TCCCTGACGG CTGCCATTGG TCCACCCTTT CATAGAGAGG CCTGCTTTGT 1260

5 TACAAAGCTC GGGTCTCCCT CCTGCAGCTC GGTAAAGTAC CCGAGGCCTC TCTTAAGATG 1320
TCCAGGGCCC CAGGCCCCGCG GGCACAGCCA GCCCAAACCT TGGGCCCTGG AAGAGTCCTC 1380
CACCCCATCA CTAGAGTGCT CTGACCCTGG GCTTTCACGG GCCCCATTCC ACCGCCTCCC 1440
CAACTTGAGC CTGTGACCTT GGGACCAAAG GGGGAGTCCC TCGTCTCTTG TGA CT CAGCA 1500
10 GAGGCAGTGG CCACGTT CAG GGAGGGGCGG GCTGGCCTGG AGGCTCAGCC CACCCTCCAG 1560
CTTTTCCTCA GGGTGTCTG AGGTCCAAGA TTCTGGAGCA ATCTGACCCT TCTCCAAAGG 1620
CTCTGTTATC AGCTGGGCAG TGCCAGCCAA TCCCTGGCCA TTTGGCCCCA GGGGACGTGG 1680
15 GCCCTG 1686

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

30 GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC 60
35 TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120
CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180
AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240
40 CCCGATGTGA ACATGCTGCA CGTGTTTGT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300
AAGAAGAAGC TGAAATACCT GCCCTACAAT CACCAGCACG AATACTTCTT CCTGATTGGG 360
45 CCGCCGCTGC TCATCCCCAT GTATTTCCAG TACCAGATCA TCATGACCAT GATCGTCCAT 420
AAGAACTGGG TGGACCTGGC CTGGGCCGTC AGCTACTACA TCCGGTTCTT CATCACCTAC 480
ATCCCTTTCT ACGGCATCCT GGGAGCCCTC CTTTTCCTCA ACTTCATCAG GTTCCTGGAG 540
50 AGCCACTGGT TTGTGTGGGT CACACAGATG AATCACATCG TCATGGAGAT TGACCAGGAG 600
GCCTACCGTG ACTGGTTCAG TAGCCAGCTG ACAGCCACCT GCAACGTGGA GCAGTCCTTC 660
TTCAACGACT GGTTCAGTGG ACACCTTAAC TTCCAGATTG AGCACCACCT CTTCCCCACC 720
55 ATGCCCCGGC ACAACTTACA CAAGATCGCC CCGCTGGTGA AGTCTCTATG TGCCAAGCAT 780
GGCATTGAAT ACCAGGAGAA GCCGCTACTG AGGGCCCTGC TGGACATCAT CAGGTCCCTG 840
60 AAGAAGTCTG GGAAGCTGTG GCTGGACGCC TACCTTCACA AATGAAGCCA CAGCCCCCGG 900
GACACCGTGG GGAAGGGGTG CAGGTGGGGT GATGGCCAGA GGAATGATGG GCTTTTGTTT 960
65 TGAGGGGTGT CCGAGAGGCT GGTGTATGCA CTGCTCACGG ACCCATGTT GGATCTTTCT 1020

5 CCCTTTCTCC TCTCCTTTTT CTCTTCACAT CTCCCCATA GCACCCTGCC CTCATGGGAC 1080
 CTGCCCTCCC TCAGCCGTCA GCCATCAGCC ATGGCCCTCC CAGTGCCTCC TAGCCCCTTC 1140
 TTCCAAGGAG CAGAGAGGTG GCCACCGGGG GTGGCTCTGT CCTACCTCCA CTCTCTGCCC 1200
 CTAAAGATGG GAGGAGACCA GCGGTCCATG GGTCTGGCCT GTGAGTCTCC CTTGCAGCC 1260
 10 TGGTCACTAG GCATCACCCC CGCTTTGGTT CTTCAGATGC TCTTGGGGTT CATAGGGGCA 1320
 GGTCTAGTC GGGCAGGGCC CCTGACCCTC CCGGCCTGGC TTCACTCTCC CTGACGGCTG 1380
 CCATTGGTCC ACCCTTTTCAT AGAGAGGCCT GCTTTGTAC AAAGCTCGGG TCTCCCTCCT 1440
 15 GCAGCTCGGT TAAGTACCCG AGGCCTCTCT TAAGATGTCC AGGGCCCCAG GCCCGCGGGC 1500
 ACAGCCAGCC CAAACCTTGG GCCCTGGAAG AGTCTCCAC CCCATCACTA GAGTGCTCTG 1560
 ACCCTGGGCT TTCACGGGCC CCATTCCACC GCCTCCCCAA CTTGAGCCTG TGACCTTGGG 1620
 20 ACCAAAGGGG GAGTCCCTCG TCTCTTGTGA CTCAGCAGAG GCAGTGGCCA CGTTCAGGGA 1680
 GGGGCCGGCT GGCCTGGAGG CTCAGCCCAC CCTCCAGCTT TTCCTCAGGG TGTCTGAGG 1740
 25 TCCAAGATTC TGGAGCAATC TGACCCTTCT CCAAAGGCTC TGTATCAGC TGGGCAGTGC 1800
 CAGCCAATCC CTGGCCATTT GGCCCCAGGG GACGTGGGCC CTG 1843

30 (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2257 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 253538a)

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAGGGACCTA CCCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG 60
 45 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 50 CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGAG CCTGGCTCAC CTTTGGGTC 420
 55 TTTGGGACGT CCTTTTGGCC CTTCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGCAG 480
 GCCCAAGCTG GATGGCTGCA ACATGATTAT GGCCACCTGT CTGTCTACAG AAAACCCAAG 540
 60 TGGAACCACC TTGTCCACAA ATTCGTCATT GGCCACTTAA AGGGTGCCTC TGCCAAGTGG 600
 TGGAATCATC GCCACTTCCA GCACCACGCC AAGCCTAACA TCTTCCACAA GGATCCCGAT 660
 65 GTGAACATGC TGCACGTGTT TGTTCTGGGC GAATGGCAGC CCATCGAGTA CGGCAAGAAG 720

5 AAGCTGAAAT ACCTGCCCTA CAATCACCAG CACGAATACT TCTTCCTGAT TGGGCCGCCG 780
 CTGCTCATCC CCATGTATTT CCAGTACCAG ATCATCATGA CCATGATCGT CCATAAGAAC 840
 TGGGTGGACC TGGCCTGGGC CGTCAGCTAC TACATCCGGT TCTTCATCAC CTACATCCCT 900
 10 TTCTACGGCA TCCTGGGAGC CCTCCTTTTC CTCAACTTCA TCAGGTTCCCT GGAGAGCCAC 960
 TGGTTTGTGT GGGTCACACA GATGAATCAC ATCGTCATGG AGATTGACCA GGAGGCCTAC 1020
 CGTGACTGGT TCAGTAGCCA GCTGACAGCC ACCTGCAACG TGGAGCAGTC CTTCTTCAAC 1080
 GACTGGTTCA GTGGACACCT TAACTTCCAG ATTGAGCACC ACCTCTTCCC CACCATGCCC 1140
 15 CGGCACAACT TACACAAGAT CGCCCCGCTG GTGAAGTCTC TATGTGCCAA GCATGGCATT 1200
 GAATACCAGG AGAAGCCGCT ACTGAGGGCC CTGCTGGACA TCATCAGGTC CCTGAAGAAG 1260
 20 TCTGGGAAGC TGTGGCTGGA CGCCTACCTT CACAAATGAA GCCACAGCCC CCGGGACACC 1320
 GTGGGGAAGG GGTGCAGGTG GGGTGATGGC CAGAGGAATG ATGGGCTTTT GTTCTGAGGG 1380
 GTGTCCGAGA GGCTGGTGTA TGCACTGCTC ACGGACCCCA TGTGGATCT TTCTCCCTTT 1440
 25 CTCCTCTCCT TTTTCTCTC ACATCTCCCC CATAGCACCC TGCCCTCATG GGACCTGCCC 1500
 TCCCTCAGCC GTCAGCCATC AGCCATGGCC CTCCCAGTGC CTCCTAGCCC CTTCTTCCAA 1560
 30 GGAGCAGAGA GGTGGCCACC GGGGGTGGCT CTGTCCTACC TCCACTCTCT GCCCCTAAAG 1620
 ATGGGAGGAG ACCAGCGGTC CATGGGTCTG GCCTGTGAGT CTCCCCTTGC AGCCTGGTCA 1680
 CTAGGCATCA CCCCCGCTTT GGTTCTTCAG ATGCTCTTGG GGTTCATAGG GGCAGGTCCT 1740
 35 AGTCGGGCAG GGCCCTGAC CCTCCCGGCC TGGCTTCACT CTCCTGACG GCTGCCATTG 1800
 GTCCACCCTT TCATAGAGAG GCCTGCTTTG TTACAAAGCT CGGGTCTCCC TCCTGCAGCT 1860
 40 CGGTAAAGTA CCCGAGGCCT CTCTTAAGAT GTCCAGGGCC CCAGGCCCGC GGGCACAGCC 1920
 AGCCCAAACC TTGGGCCCTG GAAGAGTCCT CCACCCCATC ACTAGAGTGC TCTGACCCTG 1980
 GGCTTTCACG GGCCCATTC CACCGCTCC CCAACTTGAG CCTGTGACCT TGGGACCAA 2040
 45 GGGGGAGTCC CTCGTCTCTT GTGACTCAGC AGAGGCAGTG GCCACGTTCA GGGAGGGGCC 2100
 GGCTGGCCTG GAGGCTCAGC CCACCCTCCA GCTTTTCCTC AGGGTGTCTT GAGGTCCAAG 2160
 50 ATTCTGGAGC AATCTGACCC TTCTCAAAG GCTCTGTTAT CAGCTGGGCA GTGCCAGCCA 2220
 ATCCCTGGCC ATTTGGCCCC AGGGGACGTG GGCCCTG 2257

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | His | Ala | Asp | Arg | Arg | Arg | Glu | Ile | Leu | Ala | Lys | Tyr | Pro | Glu | Ile | |
| | 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| 5 | Lys | Ser | Leu | Met | Lys | Pro | Asp | Pro | Asn | Leu | Ile | Trp | Ile | Ile | Ile | |
| | | | | | 20 | | | | | 25 | | | | | 30 | |
| | Met | Met | Val | Leu | Thr | Gln | Leu | Gly | Ala | Phe | Tyr | Ile | Val | Lys | Asp | |
| | | | | | 35 | | | | | 40 | | | | | 45 | |
| | Leu | Asp | Trp | Lys | Trp | Val | Ile | Phe | Gly | Ala | Tyr | Ala | Phe | Gly | Ser | |
| | | | | | 50 | | | | | 55 | | | | | 60 | |
| 10 | Cys | Ile | Asn | His | Ser | Met | Thr | Leu | Ala | Ile | His | Glu | Ile | Ala | His | |
| | | | | | 65 | | | | | 70 | | | | | 75 | |
| | Asn | Ala | Ala | Phe | Gly | Asn | Cys | Lys | Ala | Met | Trp | Asn | Arg | Trp | Phe | |
| | | | | | 80 | | | | | 85 | | | | | 90 | |
| 15 | Gly | Met | Phe | Ala | Asn | Leu | Pro | Ile | Gly | Ile | Pro | Tyr | Ser | Ile | Ser | |
| | | | | | 95 | | | | | 100 | | | | | 105 | |
| | Phe | Lys | Arg | Tyr | His | Met | Asp | His | His | Arg | Tyr | Leu | Gly | Ala | Asp | |
| | | | | | 110 | | | | | 115 | | | | | 120 | |
| | Gly | Val | Asp | Val | Asp | Ile | Pro | Thr | Asp | Phe | Glu | Gly | Trp | Phe | Phe | |
| | | | | | 125 | | | | | 130 | | | | | 135 | |
| 20 | Cys | Thr | Ala | Phe | Arg | Lys | Phe | Ile | Trp | Val | Ile | Leu | Gln | Pro | Leu | |
| | | | | | 140 | | | | | 145 | | | | | 150 | |
| | Phe | Tyr | Ala | Phe | Arg | Pro | Leu | Phe | Ile | Asn | Pro | Lys | Pro | Ile | Thr | |
| | | | | | 155 | | | | | 160 | | | | | 165 | |
| 25 | Tyr | Leu | Glu | Val | Ile | Asn | Thr | Val | Ala | Gln | Val | Thr | Phe | Asp | Ile | |
| | | | | | 170 | | | | | 175 | | | | | 180 | |
| | Leu | Ile | Tyr | Tyr | Phe | Leu | Gly | Ile | Lys | Ser | Leu | Val | Tyr | Met | Leu | |
| | | | | | 185 | | | | | 190 | | | | | 195 | |
| | Ala | Ala | Ser | Leu | Leu | Gly | Leu | Gly | Leu | His | Pro | Ile | Ser | Gly | His | |
| | | | | | 200 | | | | | 205 | | | | | 210 | |
| 30 | Phe | Ile | Ala | Glu | His | Tyr | Met | Phe | Leu | Lys | Gly | His | Glu | Thr | Tyr | |
| | | | | | 215 | | | | | 220 | | | | | 225 | |
| | Ser | Tyr | Tyr | Gly | Pro | Leu | Asn | Leu | Leu | Thr | Phe | Asn | Val | Gly | Tyr | |
| | | | | | 230 | | | | | 235 | | | | | 240 | |
| 35 | His | Asn | Glu | His | His | Asp | Phe | Pro | Asn | Ile | Pro | Gly | Lys | Ser | Leu | |
| | | | | | 245 | | | | | 250 | | | | | 255 | |
| | Pro | Leu | Val | Arg | Lys | Ile | Ala | Ala | Glu | Tyr | Tyr | Asp | Asn | Leu | Pro | |
| | | | | | 260 | | | | | 265 | | | | | 270 | |
| | His | Tyr | Asn | Ser | Trp | Ile | Lys | Val | Leu | Tyr | Asp | Phe | Val | Met | Asp | |
| | | | | | 275 | | | | | 280 | | | | | 285 | |
| 40 | Asp | Thr | Ile | Ser | Pro | Tyr | Ser | Arg | Met | Lys | Arg | His | Gln | Lys | Gly | |
| | | | | | 290 | | | | | 295 | | | | | 300 | |
| | Glu | Met | Val | Leu | Glu | Xaa | Ile | Ser | Leu | Val | Pro | Lys | Gly | Phe | Phe | |
| | | | | | 305 | | | | | 310 | | | | | 315 | |
| 45 | Ser | Lys | Thr | Leu | Asp | Asp | Lys | Met | Glu | Phe | Leu | His | Tyr | Xaa | Thr | |
| | | | | | 320 | | | | | 325 | | | | | 330 | |
| | Xaa | Asp | Gln | Xaa | Cys | Ser | Glu | Ala | Pro | Leu | Ala | Gln | Phe | Gln | Ser | |
| | | | | | 335 | | | | | 340 | | | | | 345 | |
| | Lys | Ser | Ser | Val | Ile | Pro | Arg | Ser | Glu | Ser | Gly | Phe | Xaa | Thr | Val | |
| | | | | | 350 | | | | | 355 | | | | | 360 | |
| 50 | Ser | Leu | Thr | Leu | Tyr | Cys | Ser | Val | Ser | Leu | Thr | Gly | Asn | Leu | Xaa | |
| | | | | | 365 | | | | | 370 | | | | | 375 | |
| | Leu | Val | Tyr | Tyr | Arg | His | Xaa | Gly | Cys | Phe | Thr | His | Val | Cys | His | |
| | | | | | 380 | | | | | 385 | | | | | 390 | |
| 55 | Phe | Ile | Ser | Ile | Ser | Phe | Lys | Lys | Leu | Leu | Lys | Ser | Tyr | Phe | Ala | |
| | | | | | 400 | | | | | 405 | | | | | 410 | |
| | Arg | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:35:

- 60 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 65

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2153526)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

5
Tyr Leu Leu Arg Pro Leu Leu Pro His Leu Cys Ala Thr Ile Gly
1 5 10 15
Ala Glu Ser Phe Leu Gly Leu Phe Phe Ile Val Arg Phe Leu Glu
20 25 30
10 Ser Asn Trp Phe Val Trp Val Thr Gln Met Asn His Ile Pro Met
35 40 45
His Ile Asp His Asp Arg Asn Met Asp Trp Val Ser Thr Gln Leu
50 55 60
Gln Ala Thr Cys Asn Val His Lys Ser Ala Phe Asn Asp Trp Phe
15 65 70 75
Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
80 85 90
Met Pro Arg His Asn Tyr His Lys Val Ala Pro Leu Val Gln Ser
95 100 105
20 Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser Lys Pro Leu Leu
110 115 120
Ser Ala Phe Ala Asp Ile Ile His Ser Leu Lys Glu Ser Gly Gln
125 130 135
25 Leu Trp Leu Asp Ala Tyr Leu His Gln Xaa Gln Gln Pro Pro Cys
140 145 150
Pro Val Trp Lys Lys Arg Arg Lys Thr Leu Glu Pro Arg Gln Arg
155 160 165
Gly Ala Xaa Gly Thr Met Pro Leu Xaa Phe Asn Thr Gln Arg Gly
170 175 180
30 Leu Gly Leu Gly Thr Xaa Ser Leu Xaa Leu Lys Leu Leu Pro Phe
185 190 195
Ile Phe Xaa Pro Gln Phe Xaa Asp Pro Lys Trp Gly Val Asp Thr
200 205 210
35 Glu Val Pro Arg Arg Glu Gly Ala
215

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

50
Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
1 5 10 15
55 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
20 25 30
Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
35 40 45
Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
60 50 55 60
Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
65 70 75
Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xaa
80 85

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
1 5 10 15
Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
20 25 30
Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
35 40 45
Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
50 55 60
Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
25 65 70 75
Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro
80 85 90
Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
95 100 105
30 Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
110 115 120
Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
125 130 135
Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
35 140 145 150
Cys Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp Leu
155 160 165
Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp
170 175 180
40 Asn His Leu Leu His His Phe Val Ile Gly His Leu Lys Gly Ala
185 190 195
Pro Ala Ser Trp Trp Asn His Met His Phe Gln His His Ala Lys
200 205 210
Pro Asn Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro Phe
45 215 220 225
Phe Phe Ala Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln
230 235 240
Lys Lys Lys Tyr Met Pro Tyr Asn His Gln His Xaa Tyr Phe Phe
245 250 255
50 Leu Ile Gly Pro Pro Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr
260 265 270
Ile Phe Tyr Phe Val Ile Gln Arg Lys Lys Trp Val Asp Leu Ala
275 280 285
Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly Leu Pro Leu Ser
55 290 295 300
Thr Ala Asn Ala Ser Lys
305

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | His | Leu | Lys | Gly | Ala | Ser | Ala | Asn | Trp | Trp | Asn | His | Arg | His | Phe | |
| | 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| 10 | Gln | His | His | Ala | Lys | Pro | Asn | Ile | Phe | His | Lys | Asp | Pro | Asp | Val | |
| | | | | | 20 | | | | | 25 | | | | | 30 | |
| | Asn | Met | Leu | His | Val | Phe | Val | Leu | Gly | Glu | Trp | Gln | Pro | Ile | Glu | |
| | | | | | 35 | | | | | 40 | | | | | 45 | |
| 15 | Tyr | Gly | Lys | Lys | Lys | Leu | Lys | Tyr | Leu | Pro | Tyr | Asn | His | Gln | His | |
| | | | | | 50 | | | | | 55 | | | | | 60 | |
| | Glu | Tyr | Phe | Phe | Leu | Ile | Gly | Pro | Pro | Leu | Leu | Ile | Pro | Met | Tyr | |
| | | | | | 65 | | | | | 70 | | | | | 75 | |
| | Phe | Gln | Tyr | Gln | Ile | Ile | Met | Thr | Met | Ile | Val | His | Lys | Asn | Trp | |
| | | | | | 80 | | | | | 85 | | | | | 90 | |
| 20 | Val | Asp | Leu | Ala | Trp | Ala | Val | Ser | Tyr | Tyr | Ile | Arg | Phe | Phe | Ile | |
| | | | | | 95 | | | | | 100 | | | | | 105 | |
| | Thr | Tyr | Ile | Pro | Phe | Tyr | Gly | Ile | Leu | Gly | Ala | Leu | Leu | Phe | Leu | |
| | | | | | 110 | | | | | 115 | | | | | 120 | |
| 25 | Asn | Phe | Ile | Arg | Phe | Leu | Glu | Ser | His | Trp | Phe | Val | Trp | Val | Thr | |
| | | | | | 125 | | | | | 130 | | | | | 135 | |
| | Gln | Met | Asn | His | Ile | Val | Met | Glu | Ile | Asp | Gln | Glu | Ala | Tyr | Arg | |
| | | | | | 140 | | | | | 145 | | | | | 150 | |
| | Asp | Trp | Phe | Ser | Ser | Gln | Leu | Thr | Ala | Thr | Cys | Asn | Val | Glu | Gln | |
| | | | | | 155 | | | | | 160 | | | | | 165 | |
| 30 | Ser | Phe | Phe | Asn | Asp | Trp | Phe | Ser | Gly | His | Leu | Asn | Phe | Gln | Ile | |
| | | | | | 170 | | | | | 175 | | | | | 180 | |
| | Glu | His | His | Leu | Phe | Pro | Thr | Met | Pro | Arg | His | Asn | Leu | His | Lys | |
| | | | | | 185 | | | | | 190 | | | | | 195 | |
| 35 | Ile | Ala | Pro | Leu | Val | Lys | Ser | Leu | Cys | Ala | Lys | His | Gly | Ile | Glu | |
| | | | | | 200 | | | | | 205 | | | | | 210 | |
| | Tyr | Gln | Glu | Lys | Pro | Leu | Leu | Arg | Ala | Leu | Leu | Asp | Ile | Ile | Arg | |
| | | | | | 215 | | | | | 220 | | | | | 225 | |
| | Ser | Leu | Lys | Lys | Ser | Gly | Lys | Leu | Trp | Leu | Asp | Ala | Tyr | Leu | His | |
| | | | | | 230 | | | | | 235 | | | | | 240 | |
| 40 | Lys | Xaa | Ser | His | Ser | Pro | Arg | Asp | Thr | Val | Gly | Lys | Gly | Cys | Arg | |
| | | | | | 245 | | | | | 250 | | | | | 255 | |
| | Trp | Gly | Asp | Gly | Gln | Arg | Asn | Asp | Gly | Leu | Leu | Phe | Xaa | Gly | Val | |
| | | | | | 260 | | | | | 265 | | | | | 270 | |
| 45 | Ser | Glu | Arg | Leu | Val | Tyr | Ala | Leu | Leu | Thr | Asp | Pro | Met | Leu | Asp | |
| | | | | | 275 | | | | | 280 | | | | | 285 | |
| | Leu | Ser | Pro | Phe | Leu | Leu | Ser | Phe | Phe | Ser | Ser | His | Leu | Pro | His | |
| | | | | | 290 | | | | | 295 | | | | | 300 | |
| | Ser | Thr | Leu | Pro | Ser | Trp | Asp | Leu | Pro | Ser | Leu | Ser | Arg | Gln | Pro | |
| | | | | | 305 | | | | | 310 | | | | | 315 | |
| 50 | Ser | Ala | Met | Ala | Leu | Pro | Val | Pro | Pro | Ser | Pro | Phe | Phe | Gln | Gly | |
| | | | | | 320 | | | | | 325 | | | | | 330 | |
| | Ala | Glu | Arg | Trp | Pro | Pro | Gly | Val | Ala | Leu | Ser | Tyr | Leu | His | Ser | |
| | | | | | 335 | | | | | 340 | | | | | 345 | |
| | Leu | Pro | Leu | Lys | Met | Gly | Gly | Asp | Gln | Arg | Ser | Met | Gly | Leu | Ala | |
| 55 | | | | | 350 | | | | | 355 | | | | | 360 | |
| | Cys | Glu | Ser | Pro | Leu | Ala | Ala | Trp | Ser | Leu | Gly | Ile | Thr | Pro | Ala | |
| | | | | | 365 | | | | | 370 | | | | | 375 | |
| | Leu | Val | Leu | Gln | Met | Leu | Leu | Gly | Phe | Ile | Gly | Ala | Gly | Pro | Ser | |
| | | | | | 380 | | | | | 385 | | | | | 390 | |
| 60 | Arg | Ala | Gly | Pro | Leu | Thr | Leu | Pro | Ala | Trp | Leu | His | Ser | Pro | Xaa | |
| | | | | | 400 | | | | | 405 | | | | | 410 | |
| | Arg | Leu | Pro | Leu | Val | His | Pro | Phe | Ile | Glu | Arg | Pro | Ala | Leu | Leu | |
| | | | | | 415 | | | | | 420 | | | | | 425 | |
| 65 | Gln | Ser | Ser | Gly | Leu | Pro | Pro | Ala | Ala | Arg | Leu | Ser | Thr | Arg | Gly | |
| | | | | | 430 | | | | | 435 | | | | | 440 | |

5 Leu Ser Xaa Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala Ser
 445 450 455
 Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser
 460 465 470
 Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro
 475 480 485
 Thr Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu
 490 495 500
 10 Leu Xaa Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly
 505 510 515
 Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val
 520 525 530
 Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala
 535 540 545
 15 Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala
 550 555 560
 Pro Gly Asp Val Gly Pro Xaa
 565

20

(2) INFORMATION FOR SEQ ID NO:39:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 619 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: amino acid (Translation of Contig 2535)
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

35 Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
 1 5 10 15
 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
 20 25 30
 40 Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
 35 40 45
 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
 50 55 60
 Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
 65 70 75
 45 Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His Val Phe Val
 80 85 90
 Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys Lys Leu Lys
 95 100 105
 50 Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu Ile Gly
 110 115 120
 Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile Met
 125 130 135
 Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val
 140 145 150
 55 Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly
 155 160 165
 Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu
 170 175 180
 Ser His Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met
 185 190 195
 60 Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu
 200 205 210
 Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe
 215 220 225
 65 Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr

-170-

SUBSTITUTE SHEET

| | | | | | | |
|--|-----|-----|-----|-----|-----|-----|
| | | 230 | | 235 | | 240 |
| | Met | Pro | Arg | His | Asn | Leu |
| | | | | | His | Lys |
| | | | | | Ile | Ala |
| | | | | | Pro | Leu |
| | | | | | Val | Lys |
| | | | | | Ser | |
| | | | | | 245 | 255 |
| | Leu | Cys | Ala | Lys | His | Gly |
| | | | | | Ile | Glu |
| | | | | | Tyr | Gln |
| | | | | | Glu | Lys |
| | | | | | Pro | Leu |
| | | | | | Leu | |
| | | | | | 260 | 270 |
| | Arg | Ala | Leu | Leu | Asp | Ile |
| | | | | | Ile | Arg |
| | | | | | Ser | Leu |
| | | | | | Lys | Lys |
| | | | | | Ser | Gly |
| | | | | | Lys | |
| | | | | | 275 | 285 |
| | Leu | Trp | Leu | Asp | Ala | Tyr |
| | | | | | Leu | His |
| | | | | | Lys | Xaa |
| | | | | | Ser | His |
| | | | | | Ser | Pro |
| | | | | | Arg | |
| | | | | | 290 | 300 |
| | Asp | Thr | Val | Gly | Lys | Gly |
| | | | | | Cys | Arg |
| | | | | | Trp | Gly |
| | | | | | Asp | Gly |
| | | | | | Gln | Arg |
| | | | | | Asn | |
| | | | | | 305 | 315 |
| | Asp | Gly | Leu | Leu | Phe | Xaa |
| | | | | | Gly | Val |
| | | | | | Ser | Glu |
| | | | | | Arg | Leu |
| | | | | | Val | Tyr |
| | | | | | Ala | |
| | | | | | 320 | 330 |
| | Leu | Leu | Thr | Asp | Pro | Met |
| | | | | | Leu | Asp |
| | | | | | Leu | Ser |
| | | | | | Pro | Phe |
| | | | | | Leu | Leu |
| | | | | | Ser | |
| | | | | | 335 | 345 |
| | Phe | Phe | Ser | Ser | His | Leu |
| | | | | | Pro | His |
| | | | | | Ser | Thr |
| | | | | | Leu | Pro |
| | | | | | Ser | Trp |
| | | | | | Asp | |
| | | | | | 350 | 360 |
| | Leu | Pro | Ser | Leu | Ser | Arg |
| | | | | | Gln | Pro |
| | | | | | Ser | Ala |
| | | | | | Met | Ala |
| | | | | | Leu | Pro |
| | | | | | Val | |
| | | | | | 365 | 375 |
| | Pro | Pro | Ser | Pro | Phe | Phe |
| | | | | | Gln | Gly |
| | | | | | Ala | Glu |
| | | | | | Arg | Trp |
| | | | | | Pro | Pro |
| | | | | | Gly | |
| | | | | | 380 | 390 |
| | Val | Ala | Leu | Ser | Tyr | Leu |
| | | | | | His | Ser |
| | | | | | Leu | Pro |
| | | | | | Leu | Lys |
| | | | | | Met | Gly |
| | | | | | Gly | |
| | | | | | 400 | 410 |
| | Asp | Gln | Arg | Ser | Met | Gly |
| | | | | | Leu | Ala |
| | | | | | Cys | Glu |
| | | | | | Ser | Pro |
| | | | | | Leu | Ala |
| | | | | | Ala | |
| | | | | | 415 | 425 |
| | Trp | Ser | Leu | Gly | Ile | Thr |
| | | | | | Pro | Ala |
| | | | | | Leu | Val |
| | | | | | Leu | Gln |
| | | | | | Met | Leu |
| | | | | | Leu | |
| | | | | | 430 | 440 |
| | Gly | Phe | Ile | Gly | Ala | Gly |
| | | | | | Pro | Ser |
| | | | | | Arg | Ala |
| | | | | | Gly | Pro |
| | | | | | Leu | Thr |
| | | | | | Leu | |
| | | | | | 445 | 455 |
| | Pro | Ala | Trp | Leu | His | Ser |
| | | | | | Pro | Xaa |
| | | | | | Arg | Leu |
| | | | | | Pro | Leu |
| | | | | | Val | His |
| | | | | | Pro | |
| | | | | | 460 | 470 |
| | Phe | Ile | Glu | Arg | Pro | Ala |
| | | | | | Leu | Leu |
| | | | | | Gln | Ser |
| | | | | | Ser | Gly |
| | | | | | Leu | Pro |
| | | | | | Pro | |
| | | | | | 475 | 485 |
| | Ala | Ala | Arg | Leu | Ser | Thr |
| | | | | | Arg | Gly |
| | | | | | Leu | Ser |
| | | | | | Xaa | Asp |
| | | | | | Val | Gln |
| | | | | | Gly | |
| | | | | | 490 | 500 |
| | Pro | Arg | Pro | Ala | Gly | Thr |
| | | | | | Ala | Ser |
| | | | | | Pro | Asn |
| | | | | | Leu | Gly |
| | | | | | Pro | Trp |
| | | | | | Lys | |
| | | | | | 505 | 515 |
| | Ser | Pro | Pro | Pro | His | His |
| | | | | | Xaa | Ser |
| | | | | | Ala | Leu |
| | | | | | Thr | Leu |
| | | | | | Gly | Phe |
| | | | | | His | |
| | | | | | 520 | 530 |
| | Gly | Pro | His | Ser | Thr | Ala |
| | | | | | Ser | Pro |
| | | | | | Thr | Xaa |
| | | | | | Ala | Cys |
| | | | | | Asp | Leu |
| | | | | | Gly | |
| | | | | | 535 | 545 |
| | Thr | Lys | Gly | Gly | Val | Pro |
| | | | | | Arg | Leu |
| | | | | | Leu | Xaa |
| | | | | | Leu | Ser |
| | | | | | Arg | Gly |
| | | | | | Ser | |
| | | | | | 550 | 560 |
| | Gly | His | Val | Gln | Gly | Gly |
| | | | | | Ala | Gly |
| | | | | | Trp | Pro |
| | | | | | Gly | Gly |
| | | | | | Ser | Ala |
| | | | | | His | |
| | | | | | 565 | 575 |
| | Pro | Pro | Ala | Phe | Pro | Gln |
| | | | | | Gly | Val |
| | | | | | Leu | Arg |
| | | | | | Ser | Lys |
| | | | | | Ile | Leu |
| | | | | | Glu | |
| | | | | | 580 | 590 |
| | Gln | Ser | Asp | Pro | Ser | Pro |
| | | | | | Lys | Ala |
| | | | | | Leu | Ser |
| | | | | | Ala | Gly |
| | | | | | Gln | Cys |
| | | | | | 595 | 605 |
| | Gln | Pro | Ile | Pro | Gly | His |
| | | | | | Leu | Ala |
| | | | | | Pro | Gly |
| | | | | | Asp | Val |
| | | | | | Gly | Pro |
| | | | | | Xaa | |
| | | | | | 610 | 620 |

55

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 757 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

| | | |
|----|---|-------------|
| | Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln | 1 5 10 15 |
| 5 | Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val | 20 25 30 |
| | Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg | 35 40 45 |
| 10 | Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val | 50 55 60 |
| | Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser | 65 70 75 |
| | Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro | 80 85 90 |
| 15 | Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala | 95 100 105 |
| | Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe | 110 115 120 |
| 20 | Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp | 125 130 135 |
| | Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu | 140 145 150 |
| | Cys Ala Val Leu Leu Ser Ala Val Gln Gln Ala Gln Ala Gly Trp | 155 160 165 |
| 25 | Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys | 170 175 180 |
| | Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly | 185 190 195 |
| 30 | Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala | 200 205 210 |
| | Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His | 215 220 225 |
| | Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys | 230 235 240 |
| 35 | Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe | 245 250 255 |
| | Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln | 260 265 270 |
| 40 | Ile Ile Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala | 275 280 285 |
| | Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro | 290 295 300 |
| | Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg | 305 310 315 |
| 45 | Phe Leu Glu Ser His Trp Phe Val Trp Val Thr Gln Met Asn His | 320 325 330 |
| | Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser | 335 340 345 |
| 50 | Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn | 350 355 360 |
| | Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu | 365 370 375 |
| | Phe Pro Thr Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu | 380 385 390 |
| 55 | Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys | 400 405 410 |
| | Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys | 415 420 425 |
| 60 | Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys Xaa Ser His | 430 435 440 |
| | Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp Gly Asp Gly | 445 450 455 |
| | Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu Arg Leu | 460 465 470 |
| 65 | Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe | |

| | | | | | | |
|----|-----------------|---------------------|---------------------|-----|--|-----|
| | | 475 | | 480 | | 485 |
| | Leu Leu Ser Phe | Phe Ser Ser His Leu | Pro His Ser Thr Leu | Pro | | |
| | | 490 | | 495 | | 500 |
| 5 | Ser Trp Asp Leu | Pro Ser Leu Ser Arg | Gln Pro Ser Ala Met | Ala | | |
| | | 505 | | 510 | | 515 |
| | Leu Pro Val Pro | Pro Ser Pro Phe Phe | Gln Gly Ala Glu Arg | Trp | | |
| | | 520 | | 525 | | 530 |
| | Pro Pro Gly Val | Ala Leu Ser Tyr Leu | His Ser Leu Pro Leu | Lys | | |
| | | 535 | | 540 | | 545 |
| 10 | Met Gly Gly Asp | Gln Arg Ser Met Gly | Leu Ala Cys Glu Ser | Pro | | |
| | | 550 | | 555 | | 560 |
| | Leu Ala Ala Trp | Ser Leu Gly Ile Thr | Pro Ala Leu Val Leu | Gln | | |
| | | 565 | | 570 | | 575 |
| 15 | Met Leu Leu Gly | Phe Ile Gly Ala Gly | Pro Ser Arg Ala Gly | Pro | | |
| | | 580 | | 585 | | 590 |
| | Leu Thr Leu Pro | Ala Trp Leu His Ser | Pro Xaa Arg Leu Pro | Leu | | |
| | | 595 | | 600 | | 605 |
| | Val His Pro Phe | Ile Glu Arg Pro Ala | Leu Leu Gln Ser Ser | Gly | | |
| | | 610 | | 615 | | 620 |
| 20 | Leu Pro Pro Ala | Ala Arg Leu Ser Thr | Arg Gly Leu Ser Xaa | Asp | | |
| | | 625 | | 630 | | 635 |
| | Val Gln Gly Pro | Arg Pro Ala Gly Thr | Ala Ser Pro Asn Leu | Gly | | |
| | | 640 | | 645 | | 650 |
| 25 | Pro Trp Lys Ser | Pro Pro Pro His His | Xaa Ser Ala Leu Thr | Leu | | |
| | | 655 | | 660 | | 665 |
| | Gly Phe His Gly | Pro His Ser Thr Ala | Ser Pro Thr Xaa Ala | Cys | | |
| | | 670 | | 675 | | 680 |
| | Asp Leu Gly Thr | Lys Gly Gly Val Pro | Arg Leu Leu Xaa Leu | Ser | | |
| | | 685 | | 690 | | 695 |
| 30 | Arg Gly Ser Gly | His Val Gln Gly Gly | Ala Gly Trp Pro Gly | Gly | | |
| | | 700 | | 705 | | 710 |
| | Ser Ala His Pro | Pro Ala Phe Pro Gln | Gly Val Leu Arg Ser | Lys | | |
| | | 715 | | 720 | | 725 |
| 35 | Ile Leu Glu Gln | Ser Asp Pro Ser Pro | Lys Ala Leu Leu Ser | Ala | | |
| | | 730 | | 735 | | 740 |
| | Gly Gln Cys Gln | Pro Ile Pro Gly His | Leu Ala Pro Gly Asp | Val | | |
| | | 745 | | 750 | | 755 |
| | Gly Pro Xaa | | | | | |